

SEQUENCE LISTING

<110> HIRANO, SEIKO
NONAKA, GEN
MATSUZAKI, YUMI
AKIYOSHI, NAOKI
NAKAMURA, KANAE
KIMURA, EIICHIRO
OSUMI, TSUYOSHI
MATSUI, KAZUHIKO
KAWAHARA, YOSHIO
KURAHASHI, OSAMU
NAKAMATSU, TSUYOSHI
SUGIMOTO, SHINICHI

<120> GENES FOR HEAT RESISTANT ENZYMES OF AMINO ACID BIOSYNTHETIC PATHWAY
DERIVED FROM THERMOPHILIC CORYNEFORM BACTERIA

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<140> 10/089,057

<141> 2002-04-03

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<170> PatentIn version 3.1

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Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln Val Ala Gly Asp Ala Asn	
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Leu Ala Gly His Thr Tyr Pro Asp Gln Ser Leu Tyr Pro Ala Asn Ser	
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Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr Ser Asp Val Asp Glu Arg			
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ccc tac gca gac atg atc tgg atg gag acc ggc acc cct gac ctc gag			1458
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 Asp Asp Tyr Ile Asn Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val
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 Gln Gln Val Arg Ala Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln
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 Val Ala Gly Asp Ala Asn Leu Ala Gly His Thr Tyr Pro Asp Gln Ser
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 Cys Gly His Leu Gly Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile
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Arg Ala Lys Ser Tyr Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr
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Gly Thr Pro Asp Leu Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg
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Val Phe Arg Ala Ala Arg Asp Glu Gly Ile Ala Ser Val Ala Val Tyr
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gcg gag ccg gac gca gat gcc cct ttc gtc gag tat gcc gat gag gcc      738
Ala Glu Pro Asp Ala Asp Ala Pro Phe Val Glu Tyr Ala Asp Glu Ala
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Phe Ala Leu Gly Gly Gln Thr Ser Ala Glu Ser Tyr Leu Val Ile Asp
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aag atc att gac gca gca cgc aag tcc ggt gca gac gct gtc cac ccc      834
Lys Ile Ile Asp Ala Ala Arg Lys Ser Gly Ala Asp Ala Val His Pro
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Gly Tyr Gly Phe Leu Ala Glu Asn Ala Asp Phe Ala Glu Ala Val Ile
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aac gag ggc ctg atc tgg atc gga cca tcc cct gag tcc atc cgt tcc      930
Asn Glu Gly Leu Ile Trp Ile Gly Pro Ser Pro Glu Ser Ile Arg Ser
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Leu Gly Asp Lys Val Thr Ala Arg His Ile Ala Asn Asn Ala Asn Ala
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Lys	Ile	Thr	Arg	Tyr	Arg	Glu	Pro	Ala	Gly	Pro	Gly	Val	Arg	Met	Asp		
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Val Ile Pro Phe His Ser His Ile Val Ser Asn Pro Ala Phe Val Gly	425	430	435	
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Asp Gly Glu Gly Phe Glu Val Tyr Thr Lys Trp Ile Glu Glu Val Trp	440	445	450	
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Asp Asn Pro Ile Glu Pro Phe Val Asp Ala Ala Asp Leu Asp Asp Glu	455	460	465	470
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Glu Lys Thr Pro Ser Gln Lys Val Ile Val Glu Ile Asp Gly Arg Arg	475	480	485	
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Val Glu Val Ala Leu Pro Gly Asp Leu Ala Leu Gly Gly Gly Ala Gly	490	495	500	
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Lys Val Asn Val Glu Asp Gly Ala Glu Val Ser Glu Gly Asp Thr Val	535	540	545	550
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Val Val Leu Glu Ala Met Lys Met Glu Asn Pro Val Lys Ala His Lys	555	560	565	
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Val Glu Gly Met Pro Thr Val Ile Pro Phe His Ser His Ile Val Ser
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 Ile Ala Asp Leu Lys Ala Arg Arg Ala Glu Ala His Phe Pro Met Gly
 25 30 35

gaa aag gcc gta gag aag gtc cac gcg gcc aac cgc ctc acc gcg cgc Glu Lys Ala Val Glu Lys Val His Ala Ala Asn Arg Leu Thr Ala Arg 40 45 50	500
gaa cga ctt gac tac ctg ctc gat gaa ggc tcc ttc atc gaa acc gat Glu Arg Leu Asp Tyr Leu Leu Asp Glu Gly Ser Phe Ile Glu Thr Asp 55 60 65 70	548
cag ctc gca cgc cac cgc acc acc gcg ttc ggc ctg ggc aac aag cga Gln Leu Ala Arg His Arg Thr Thr Ala Phe Gly Leu Gly Asn Lys Arg 75 80 85	596
ccg gcc acc gac ggc atc gtc acc ggc tgg ggc acc atc gac ggc cgc Pro Ala Thr Asp Gly Ile Val Thr Gly Trp Gly Thr Ile Asp Gly Arg 90 95 100	644
gag gtc tgc atc ttc tcc cag gac ggc acc gtc ttc ggt ggc gca ctc Glu Val Cys Ile Phe Ser Gln Asp Gly Thr Val Phe Gly Gly Ala Leu 105 110 115	692
ggt gag gtc tac ggc gag aag atg atc aag atc atg gag ctg gcc atc Gly Glu Val Tyr Gly Glu Lys Met Ile Lys Ile Met Glu Leu Ala Ile 120 125 130	740
gac acc ggc cgc cca ctc atc ggc ctg tac gag ggt gca ggt gcc cgc Asp Thr Gly Arg Pro Leu Ile Gly Leu Tyr Glu Gly Ala Gly Ala Arg 135 140 145 150	788
atc cag gac ggt gcg gtc tcc ctc gac ttc atc tcc cag acc ttc tat Ile Gln Asp Gly Ala Val Ser Leu Asp Phe Ile Ser Gln Thr Phe Tyr 155 160 165	836
cag aac atc cag gcc tcc ggc gtg atc ccg cag atc tcc gtg atc atg Gln Asn Ile Gln Ala Ser Gly Val Ile Pro Gln Ile Ser Val Ile Met 170 175 180	884
ggt gcc tgc gcc ggt ggc aac gcc tac ggc ccg gcc ctg acc gac ttc Gly Ala Cys Ala Gly Gly Asn Ala Tyr Gly Pro Ala Leu Thr Asp Phe 185 190 195	932
gtg gtc atg gtg gac aag acc tgc aag atg ttc gtc acc ggc ccc gat Val Val Met Val Asp Lys Thr Ser Lys Met Phe Val Thr Gly Pro Asp 200 205 210	980
gtg atc aag acc gtc acc ggc gag gag atc acc cag gag gag ctc ggc Val Ile Lys Thr Val Thr Gly Glu Glu Ile Thr Gln Glu Glu Leu Gly 215 220 225 230	1028
gga gca acc acc cac atg gtc acc gcc ggc aac tcc cac tac acc gtc Gly Ala Thr Thr His Met Val Thr Ala Gly Asn Ser His Tyr Thr Val 235 240 245	1076
gcc acc gat gag gag gcc ctc gac tgg gtc cag gac ctc atc tcc ttc Ala Thr Asp Glu Glu Ala Leu Asp Trp Val Gln Asp Leu Ile Ser Phe 250 255 260	1124
ctg ccc tcc aac aat cgc tcc tac gcc ccg gtg gag gag ttc gac gag Leu Pro Ser Asn Asn Arg Ser Tyr Ala Pro Val Glu Glu Phe Asp Glu 265 270 275	1172

gag gac ggt ggc atc gcc gag aac atc acc gcc gat gac ctg aag ctg Glu Asp Gly Gly Ile Ala Glu Asn Ile Thr Ala Asp Asp Leu Lys Leu 280 285 290	1220
gat gag atc atc ccg gat tcc gcc acc gtg ccc tat gat gtc cgc gac Asp Glu Ile Ile Pro Asp Ser Ala Thr Val Pro Tyr Asp Val Arg Asp 295 300 305 310	1268
gtc atc cag tgc ctg acc gac gac ggt gag tac ctg gag atc cag gcc Val Ile Gln Cys Leu Thr Asp Asp Gly Glu Tyr Leu Glu Ile Gln Ala 315 320 325	1316
gac cga gcc gag aat gtc gtc atc gcc ttc ggc cgc atc gag ggc cag Asp Arg Ala Glu Asn Val Val Ile Ala Phe Gly Arg Ile Glu Gly Gln 330 335 340	1364
tcc gtc ggt ttc gtc gcc aac cag ccg acc cag ttc gcc ggc tgc ctg Ser Val Gly Phe Val Ala Asn Gln Pro Thr Gln Phe Ala Gly Cys Leu 345 350 355	1412
gac atc gac tcc tcc gag aag gca gcc cgc ttc gtc cgc acc tgc gat Asp Ile Asp Ser Ser Glu Lys Ala Ala Arg Phe Val Arg Thr Cys Asp 360 365 370	1460
gcc ttc aac atc ccg atc gtc atg ctt gtc gac gtc ccc ggc ttc ctc Ala Phe Asn Ile Pro Ile Val Met Leu Val Asp Val Pro Gly Phe Leu 375 380 385 390	1508
ccc ggt gcc ggc cag gag tac ggc ggc atc ctg cgt cgt ggc gcc aaa Pro Gly Ala Gly Gln Glu Tyr Gly Gly Ile Leu Arg Arg Gly Ala Lys 395 400 405	1556
ctg ctc tac gcc tac ggt gag gcc acc gtc ccg aag atc acc gtg acc Leu Leu Tyr Ala Tyr Gly Glu Ala Thr Val Pro Lys Ile Thr Val Thr 410 415 420	1604
atg cgc aag gcc tac ggc ggt gcg tac tgt gtc atg gga tcc aag ggt Met Arg Lys Ala Tyr Gly Gly Ala Tyr Cys Val Met Gly Ser Lys Gly 425 430 435	1652
ctg ggc gca gac atc aac ctg gcc tgg ccg acc gcg cag atc gcc gtc Leu Gly Ala Asp Ile Asn Leu Ala Trp Pro Thr Ala Gln Ile Ala Val 440 445 450	1700
atg ggt gcc gcc ggc gcg gtc cag ttc atc tac cgc aag gag ctc atg Met Gly Ala Ala Gly Ala Val Gln Phe Ile Tyr Arg Lys Glu Leu Met 455 460 465 470	1748
gcc gct gat gcc aag ggc ctg gac acc gtc gcc ctg gcc cag tcc ttc Ala Ala Asp Ala Lys Gly Leu Asp Thr Val Ala Leu Ala Gln Ser Phe 475 480 485	1796
gag cgt gag tac gag gac cac atg ctc aac ccg tac ctg gcg gcc gag Glu Arg Glu Tyr Glu Asp His Met Leu Asn Pro Tyr Leu Ala Ala Glu 490 495 500	1844
cgt ggc ctc atc gac gcg gtg atc ctg ccg tcc gag acc cgt ggc cag Arg Gly Leu Ile Asp Ala Val Ile Leu Pro Ser Glu Thr Arg Gly Gln 505 510 515	1892
atc gca cgc aac ctg cgt ctg ctc aag cac aag aat gtc tcc cgc cct	1940

Ile Ala Arg Asn Leu Arg Leu Leu Lys His Lys Asn Val Ser Arg Pro
 520 525 530

gcc cgc aag cac ggc aac atg cca ctg taagcaccgc ggaccacccc 1987
 Ala Arg Lys His Gly Asn Met Pro Leu
 535 540

ctacgcccgc acccacggcc ctttgctggc aggtgcgggc gctgtgcgtt ttccgcgcct 2047

gccgacgccc ggccccctgc cctgtgatgc gatctgcgga tgtgatctgc gcccgcgcca 2107

actcccctgg ttgaaccctg c 2128

<210> 6
 <211> 543
 <212> PRT
 <213> Corynebacterium thermoaminogenes
 <400> 6

Met Thr Ile Ser Ser Pro Leu Ile Asp Val Ala Asn Leu Pro Asp Ile
 1 5 10 15

Asn Thr Thr Ala Gly Lys Ile Ala Asp Leu Lys Ala Arg Arg Ala Glu
 20 25 30

Ala His Phe Pro Met Gly Glu Lys Ala Val Glu Lys Val His Ala Ala
 35 40 45

Asn Arg Leu Thr Ala Arg Glu Arg Leu Asp Tyr Leu Leu Asp Glu Gly
 50 55 60

Ser Phe Ile Glu Thr Asp Gln Leu Ala Arg His Arg Thr Thr Ala Phe
 65 70 75 80

Gly Leu Gly Asn Lys Arg Pro Ala Thr Asp Gly Ile Val Thr Gly Trp
 85 90 95

Gly Thr Ile Asp Gly Arg Glu Val Cys Ile Phe Ser Gln Asp Gly Thr
 100 105 110

Val Phe Gly Gly Ala Leu Gly Glu Val Tyr Gly Glu Lys Met Ile Lys
 115 120 125

Ile Met Glu Leu Ala Ile Asp Thr Gly Arg Pro Leu Ile Gly Leu Tyr
 130 135 140

Glu Gly Ala Gly Ala Arg Ile Gln Asp Gly Ala Val Ser Leu Asp Phe
 145 150 155 160

Ile Ser Gln Thr Phe Tyr Gln Asn Ile Gln Ala Ser Gly Val Ile Pro
165 170 175

Gln Ile Ser Val Ile Met Gly Ala Cys Ala Gly Gly Asn Ala Tyr Gly
180 185 190

Pro Ala Leu Thr Asp Phe Val Val Met Val Asp Lys Thr Ser Lys Met
195 200 205

Phe Val Thr Gly Pro Asp Val Ile Lys Thr Val Thr Gly Glu Glu Ile
210 215 220

Thr Gln Glu Glu Leu Gly Gly Ala Thr Thr His Met Val Thr Ala Gly
225 230 235 240

Asn Ser His Tyr Thr Val Ala Thr Asp Glu Glu Ala Leu Asp Trp Val
245 250 255

Gln Asp Leu Ile Ser Phe Leu Pro Ser Asn Asn Arg Ser Tyr Ala Pro
260 265 270

Val Glu Glu Phe Asp Glu Glu Asp Gly Gly Ile Ala Glu Asn Ile Thr
275 280 285

Ala Asp Asp Leu Lys Leu Asp Glu Ile Ile Pro Asp Ser Ala Thr Val
290 295 300

Pro Tyr Asp Val Arg Asp Val Ile Gln Cys Leu Thr Asp Asp Gly Glu
305 310 315 320

Tyr Leu Glu Ile Gln Ala Asp Arg Ala Glu Asn Val Val Ile Ala Phe
325 330 335

Gly Arg Ile Glu Gly Gln Ser Val Gly Phe Val Ala Asn Gln Pro Thr
340 345 350

Gln Phe Ala Gly Cys Leu Asp Ile Asp Ser Ser Glu Lys Ala Ala Arg
355 360 365

Phe Val Arg Thr Cys Asp Ala Phe Asn Ile Pro Ile Val Met Leu Val
370 375 380

Asp Val Pro Gly Phe Leu Pro Gly Ala Gly Gln Glu Tyr Gly Gly Ile
385 390 395 400

Leu Arg Arg Gly Ala Lys Leu Leu Tyr Ala Tyr Gly Glu Ala Thr Val

405

410

415

Pro Lys Ile Thr Val Thr Met Arg Lys Ala Tyr Gly Gly Ala Tyr Cys
 420 425 430

Val Met Gly Ser Lys Gly Leu Gly Ala Asp Ile Asn Leu Ala Trp Pro
 435 440 445

Thr Ala Gln Ile Ala Val Met Gly Ala Ala Gly Ala Val Gln Phe Ile
 450 455 460

Tyr Arg Lys Glu Leu Met Ala Ala Asp Ala Lys Gly Leu Asp Thr Val
 465 470 475 480

Ala Leu Ala Gln Ser Phe Glu Arg Glu Tyr Glu Asp His Met Leu Asn
 485 490 495

Pro Tyr Leu Ala Ala Glu Arg Gly Leu Ile Asp Ala Val Ile Leu Pro
 500 505 510

Ser Glu Thr Arg Gly Gln Ile Ala Arg Asn Leu Arg Leu Leu Lys His
 515 520 525

Lys Asn Val Ser Arg Pro Ala Arg Lys His Gly Asn Met Pro Leu
 530 535 540

<210> 7
 <211> 2076
 <212> DNA
 <213> Corynebacterium thermoaminogenes

<220>
 <221> CDS
 <222> (412) .. (2022)
 <223>

<400> 7
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 ccctgggtga accctgccac ataccctgag tcgcacctgg gtgggggtcac tttccacctc 120
 acgggggggga ggaggtcaca taggccatac gctgcacttt tgatgaagtg tgggcagatc 180
 gaccggggcaa atctgggaaa taaggggcct ggtgaactag cattcccctt agcgaagggt 240
 gagcatcgcg gaccccgga tgtcccaacc ggtcgtaaatt tcatgtgccg ccacagtccc 300
 ctcaccaggg gatcggaacc agcccagcct gattccggcg tgacggacct caccgtgaac 360
 aagtccccgc attactcaca gaactcacac caggatttag actaagaaac c atg'act 417
 Met Thr
 1

gca gca acg aca gca cct gat ctg acc acc acc gcc ggc aaa ctc gcg Ala Ala Thr Thr Ala Pro Asp Leu Thr Thr Thr Ala Gly Lys Leu Ala 5 10 15	465
gat ctc cgc gcc cgc ctt tcc gag acc cag gcc ccc atg ggt cag gcc Asp Leu Arg Ala Arg Leu Ser Glu Thr Gln Ala Pro Met Gly Gln Ala 20 25 30	513
tcc gtg gag aag gtg cac gag gca ggg aag aag acc gca cgc gag cgc Ser Val Glu Lys Val His Glu Ala Gly Lys Lys Thr Ala Arg Glu Arg 35 40 45 50	561
atc gag tac ctg ctc gat gag ggc tcc ttc gtt gag gtc gat gcc ctc Ile Glu Tyr Leu Leu Asp Glu Gly Ser Phe Val Glu Val Asp Ala Leu 55 60 65	609
gcc cgc cac cgt tcc aag aac ttc ggc ctg gac tcc aag cgc ccg gtc Ala Arg His Arg Ser Lys Asn Phe Gly Leu Asp Ser Lys Arg Pro Val 70 75 80	657
acc gac ggt gtg gtc acc ggt tac ggc acc atc gac gga cgc aag gtc Thr Asp Gly Val Val Thr Gly Tyr Gly Thr Ile Asp Gly Arg Lys Val 85 90 95	705
tgc gtc ttc tcc cag gac ggc gct atc ttc ggc ggt gcc ctc ggt gag Cys Val Phe Ser Gln Asp Gly Ala Ile Phe Gly Gly Ala Leu Gly Glu 100 105 110	753
gtc tac ggc gag aag atc gtc aag atc atg gac ctg gcc atc aag acc Val Tyr Gly Glu Lys Ile Val Lys Ile Met Asp Leu Ala Ile Lys Thr 115 120 125 130	801
ggt gtc ccc ctc atc ggc atc aac gag ggc gcc ggc gcc cgc atc cag Gly Val Pro Leu Ile Gly Ile Asn Glu Gly Ala Gly Ala Arg Ile Gln 135 140 145	849
gaa ggc gtt gtc tcc ctg ggc ctg tac tcc cag atc ttc tac cgc aac Glu Gly Val Val Ser Leu Gly Leu Tyr Ser Gln Ile Phe Tyr Arg Asn 150 155 160	897
acc cag gca tcc ggt gtc atc cca cag atc tcc ctc atc atg ggt gcc Thr Gln Ala Ser Gly Val Ile Pro Gln Ile Ser Leu Ile Met Gly Ala 165 170 175	945
tgc gcc ggt ggc cat gtg tac tcc ccc gcc ctg acc gac ttc atc atc Cys Ala Gly Gly His Val Tyr Ser Pro Ala Leu Thr Asp Phe Ile Ile 180 185 190	993
atg gtg gac aag acc tcc aag atg ttc atc acc ggc ccc gac gtg atc Met Val Asp Lys Thr Ser Lys Met Phe Ile Thr Thr Gly Pro Asp Val Ile 195 200 205 210	1041
aag acc gtc acc ggc gag gag gtc acc cag gag gaa ctg ggt ggt gcc Lys Thr Val Thr Gly Glu Glu Val Thr Gln Glu Glu Leu Gly Gly Ala 215 220 225	1089
tac acc cac atg gcc cag tcc ggc acc tcg cac tac acc gca gcc gat Tyr Thr His Met Ala Gln Ser Gly Thr Ser His Tyr Thr Ala Ala Asp 230 235 240	1137

gac tcc gat gcc ctc gac tgg gtc cgt gag ctg gtc agc tac ctg ccg Asp Ser Asp Ala Leu Asp Trp Val Arg Glu Leu Val Ser Tyr Leu Pro 245 250 255	1185
tcc aac aac cgt gcg gag acc cca cgc cag gac gcc gac atc atg gtg Ser Asn Asn Arg Ala Glu Thr Pro Arg Gln Asp Ala Asp Ile Met Val 260 265 270	1233
ggc tcc atc aag gag aac atc acc gag acc gac ctc gaa ctc gac acc Gly Ser Ile Lys Glu Asn Ile Thr Glu Thr Asp Leu Glu Leu Asp Thr 275 280 285 290	1281
ctg atc ccg gat tcc ccg aac cag ccg tac gac atg aag gac gtc atc Leu Ile Pro Asp Ser Pro Asn Gln Pro Tyr Asp Met Lys Asp Val Ile 295 300 305	1329
acc cgc atc gtc gat gat gcc gag ttc ttc gag atc cag gag ggt tac Thr Arg Ile Val Asp Asp Ala Glu Phe Phe Glu Ile Gln Glu Gly Tyr 310 315 320	1377
gcc gag aac atc atc tgc ggt ttc gcc cgc gtc gag ggt cgt gcc gtg Ala Glu Asn Ile Ile Cys Gly Phe Ala Arg Val Glu Gly Arg Ala Val 325 330 335	1425
ggt atc gtg gcc aac cag ccg atg cag ttc gcc ggc tgc ctg gac atc Gly Ile Val Ala Asn Gln Pro Met Gln Phe Ala Gly Cys Leu Asp Ile 340 345 350	1473
aag gca tcc gag aag gcc gcc cgc ttc atc cgc acc tgt gac gcc ttc Lys Ala Ser Glu Lys Ala Ala Arg Phe Ile Arg Thr Cys Asp Ala Phe 355 360 365 370	1521
aac atc ccg atc atc gag ctt gtc gac gtc cca ggc ttc ctc ccg ggc Asn Ile Pro Ile Ile Glu Leu Val Asp Val Pro Gly Phe Leu Pro Gly 375 380 385	1569
acc aac cag gag ttc gac ggc atc atc cgt cgc ggc gcg aag ctg ctc Thr Asn Gln Glu Phe Asp Gly Ile Ile Arg Arg Gly Ala Lys Leu Leu 390 395 400	1617
tac gcc tac gcc gag gcc acc gtc ggc aag atc acc gtg atc acc cgc Tyr Ala Tyr Ala Glu Ala Thr Val Gly Lys Ile Thr Val Ile Thr Arg 405 410 415	1665
aag tcc tac ggc ggt gcc tac tgc gtg atg ggc tcc aag gac atg ggt Lys Ser Tyr Gly Gly Ala Tyr Cys Val Met Gly Ser Lys Asp Met Gly 420 425 430	1713
gcg gac ctc gtc ttc gca tgg ccc acc gcg cag atc gcc gtc atg ggt Ala Asp Leu Val Phe Ala Trp Pro Thr Ala Gln Ile Ala Val Met Gly 435 440 445 450	1761
gcc tcc ggt gcc gtc ggc ttc atc tac cgc aag gag ctc aag cag gct Ala Ser Gly Ala Val Gly Phe Ile Tyr Arg Lys Glu Leu Lys Gln Ala 455 460 465	1809
gca gcg gcc ggc gag gat gtc acc gcg ctg atg aag aag tac gag cag Ala Ala Ala Gly Glu Asp Val Thr Ala Leu Met Lys Lys Tyr Glu Gln 470 475 480	1857
gag tac gag gag acc ctg gtc aac ccg tac atg gct gca gag cgt ggc	1905

Glu Tyr Glu Glu Thr Leu Val Asn Pro Tyr Met Ala Ala Glu Arg Gly
 485 490 495

tac gtc gac gcc gtc atc cca cca tcc gag acc cgt ggt cag atc atc 1953
 Tyr Val Asp Ala Val Ile Pro Pro Ser Glu Thr Arg Gly Gln Ile Ile
 500 505 510

gag ggt ctg cgt ctg ctc gac cgc aag gtg gtc aac gtc ccg gcc aag 2001
 Glu Gly Leu Arg Leu Leu Asp Arg Lys Val Val Asn Val Pro Ala Lys
 515 520 525 530

aag cac ggt aac atc ccg ctg taaaccgtct tcccctccgg caccacgccg 2052
 Lys His Gly Asn Ile Pro Leu
 535

gagaaggctt tgtccgcagc tgtc 2076

<210> 8
 <211> 537
 <212> PRT
 <213> Corynebacterium thermoaminogenes

<400> 8

Met Thr Ala Ala Thr Thr Ala Pro Asp Leu Thr Thr Thr Ala Gly Lys
 1 5 10 15

Leu Ala Asp Leu Arg Ala Arg Leu Ser Glu Thr Gln Ala Pro Met Gly
 20 25 30

Gln Ala Ser Val Glu Lys Val His Glu Ala Gly Lys Lys Thr Ala Arg
 35 40 45

Glu Arg Ile Glu Tyr Leu Leu Asp Glu Gly Ser Phe Val Glu Val Asp
 50 55 60

Ala Leu Ala Arg His Arg Ser Lys Asn Phe Gly Leu Asp Ser Lys Arg
 65 70 75 80

Pro Val Thr Asp Gly Val Val Thr Gly Tyr Gly Thr Ile Asp Gly Arg
 85 90 95

Lys Val Cys Val Phe Ser Gln Asp Gly Ala Ile Phe Gly Gly Ala Leu
 100 105 110

Gly Glu Val Tyr Gly Glu Lys Ile Val Lys Ile Met Asp Leu Ala Ile
 115 120 125

Lys Thr Gly Val Pro Leu Ile Gly Ile Asn Glu Gly Ala Gly Ala Arg
 130 135 140

Ile Gln Glu Gly Val Val Ser Leu Gly Leu Tyr Ser Gln Ile Phe Tyr
 145 150 155 160

Arg Asn Thr Gln Ala Ser Gly Val Ile Pro Gln Ile Ser Leu Ile Met
 165 170 175

Gly Ala Cys Ala Gly Gly His Val Tyr Ser Pro Ala Leu Thr Asp Phe
 180 185 190

Ile Ile Met Val Asp Lys Thr Ser Lys Met Phe Ile Thr Gly Pro Asp
 195 200 205

Val Ile Lys Thr Val Thr Gly Glu Glu Val Thr Gln Glu Glu Leu Gly
 210 215 220

Gly Ala Tyr Thr His Met Ala Gln Ser Gly Thr Ser His Tyr Thr Ala
 225 230 235 240

Ala Asp Asp Ser Asp Ala Leu Asp Trp Val Arg Glu Leu Val Ser Tyr
 245 250 255

Leu Pro Ser Asn Asn Arg Ala Glu Thr Pro Arg Gln Asp Ala Asp Ile
 260 265 270

Met Val Gly Ser Ile Lys Glu Asn Ile Thr Glu Thr Asp Leu Glu Leu
 275 280 285

Asp Thr Leu Ile Pro Asp Ser Pro Asn Gln Pro Tyr Asp Met Lys Asp
 290 295 300

Val Ile Thr Arg Ile Val Asp Asp Ala Glu Phe Phe Glu Ile Gln Glu
 305 310 315 320

Gly Tyr Ala Glu Asn Ile Ile Cys Gly Phe Ala Arg Val Glu Gly Arg
 325 330 335

Ala Val Gly Ile Val Ala Asn Gln Pro Met Gln Phe Ala Gly Cys Leu
 340 345 350

Asp Ile Lys Ala Ser Glu Lys Ala Ala Arg Phe Ile Arg Thr Cys Asp
 355 360 365

Ala Phe Asn Ile Pro Ile Ile Glu Leu Val Asp Val Pro Gly Phe Leu
 370 375 380

Pro Gly Thr Asn Gln Glu Phe Asp Gly Ile Ile Arg Arg Gly Ala Lys

385 390 395 400
 Leu Leu Tyr Ala Tyr Ala Glu Ala Thr Val Gly Lys Ile Thr Val Ile
 405 410 415
 Thr Arg Lys Ser Tyr Gly Gly Ala Tyr Cys Val Met Gly Ser Lys Asp
 420 425 430
 Met Gly Ala Asp Leu Val Phe Ala Trp Pro Thr Ala Gln Ile Ala Val
 435 440 445
 Met Gly Ala Ser Gly Ala Val Gly Phe Ile Tyr Arg Lys Glu Leu Lys
 450 455 460
 Gln Ala Ala Ala Ala Gly Glu Asp Val Thr Ala Leu Met Lys Lys Tyr
 465 470 475 480
 Glu Gln Glu Tyr Glu Glu Thr Leu Val Asn Pro Tyr Met Ala Ala Glu
 485 490 495
 Arg Gly Tyr Val Asp Ala Val Ile Pro Pro Ser Glu Thr Arg Gly Gln
 500 505 510
 Ile Ile Glu Gly Leu Arg Leu Leu Asp Arg Lys Val Val Asn Val Pro
 515 520 525
 Ala Lys Lys His Gly Asn Ile Pro Leu
 530 535

<210> 9
 <211> 1643
 <212> DNA
 <213> Corynebacterium thermoaminogenes

<220>
 <221> CDS
 <222> (326)..(1363)
 <223>

<400> 9
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 tcagccaccc gccgatgaga cctgcagcga caacgggtggc ggtgctgacc tggtcagcgt 120
 ctttgagttt catatccatg tcagacagtc taaccactct ctccgacgcg tccgaacatg 180
 ctgggggtggc ggacaccatg tccgttcggg cgttgccccg acgggggaaa atcgcaggca 240
 gatgtgtccg atgtgggata aacccaccgg ttcgggcgtg tcttcgggat caatggcaca 300
 gcattaaccg tgtgggggggt ttaat atg gga gcc atg cga att gcc act ctc 352

	Met	Gly	Ala	Met	Arg	Ile	Ala	Thr	Leu	
	1				5					
acg tca ggc ggc gac tgc ccc gga ctc aat gct gtc atc agg gga atc										400
Thr Ser Gly Gly Asp Cys Pro Gly Leu Asn Ala Val Ile Arg Gly Ile	10			15		20		25		
gtc cgt acc gca agt aat gaa ttc ggt tcc acc gtc gtg ggt tat cag										448
Val Arg Thr Ala Ser Asn Glu Phe Gly Ser Thr Val Val Gly Tyr Gln		30			35			40		
gac ggc tgg gag ggc ctg ctg gcg gac cga cgt gtt cag ctc tat gac										496
Asp Gly Trp Glu Gly Leu Leu Ala Asp Arg Arg Val Gln Leu Tyr Asp		45			50			55		
gat gag gac atc gac cgc atc ctg ctc cgc ggt gga aca atc ctg ggc										544
Asp Glu Asp Ile Asp Arg Ile Leu Leu Arg Gly Gly Thr Ile Leu Gly		60			65			70		
acc ggt cgt ctc cac ccc gac aag ttc aga gcc gga atc gac cag gtc										592
Thr Gly Arg Leu His Pro Asp Lys Phe Arg Ala Gly Ile Asp Gln Val		75			80			85		
aag gcg aat ctc gcc gat gcg gga att gac gca ctc atc ccg atc ggt										640
Lys Ala Asn Leu Ala Asp Ala Gly Ile Asp Ala Leu Ile Pro Ile Gly		90			95			100		105
ggc gag ggc acc ctc aag gga gcg aag tgg ctc gcc gac aac ggc atc										688
Gly Glu Gly Thr Leu Lys Gly Ala Lys Trp Leu Ala Asp Asn Gly Ile			110				115		120	
ccc gtg gtc ggt gtc ccg aaa acc atc gac aat gat gtc aac ggc acg										736
Pro Val Val Gly Val Pro Lys Thr Ile Asp Asn Asp Val Asn Gly Thr		125				130			135	
gat ttc acc ttc ggt ttc gat tcc gcg gtc tct gtg gcc acc gac gcc										784
Asp Phe Thr Phe Gly Phe Asp Ser Ala Val Ser Val Ala Thr Asp Ala		140				145			150	
atc gac cgg ctg cac acc acg gcg gaa tcc cac aac cgt gtg atg atc										832
Ile Asp Arg Leu His Thr Thr Ala Glu Ser His Asn Arg Val Met Ile		155			160			165		
gtc gag gtc atg ggc cgc cac gtc ggt tgg atc gca ctg cat gcc ggc										880
Val Glu Val Met Gly Arg His Val Gly Trp Ile Ala Leu His Ala Gly		170			175			180		185
atg gcc ggt gga gcc cac tac acc gtc atc ccc gag gtg ccc ttc gac										928
Met Ala Gly Gly Ala His Tyr Thr Val Ile Pro Glu Val Pro Phe Asp			190			195			200	
atc tcg gag atc tgc aag cgt atg gaa cgt cgc ttc cag atg ggg gag										976
Ile Ser Glu Ile Cys Lys Arg Met Glu Arg Arg Phe Gln Met Gly Glu		205				210			215	
aag tac ggc atc atc gtc gtc gcg gag ggt gcc ctg ccc aag gag gga										1024
Lys Tyr Gly Ile Ile Val Val Ala Glu Gly Ala Leu Pro Lys Glu Gly		220				225			230	
acc atg gag ctg cgt gag ggg gag gtg gat cag ttc ggt cac aag acc										1072
Thr Met Glu Leu Arg Glu Gly Glu Val Asp Gln Phe Gly His Lys Thr										

235	240	245	
ttc acc ggc atc ggc cag cag atc gcc gac gag gtg cac agg cgt ctg			1120
Phe Thr Gly Ile Gly Gln Gln Ile Ala Asp Glu Val His Arg Arg Leu			
250	255	260	265
ggt cat gat gtc cgc acc acg gtc ctg ggc cat atc cag cgt ggt ggc			1168
Gly His Asp Val Arg Thr Thr Val Leu Gly His Ile Gln Arg Gly Gly			
270	275	280	
acc ccc acc gcc ttc gac cgt gtc ctg gcc acc cgg tac ggt gtc cgc			1216
Thr Pro Thr Ala Phe Asp Arg Val Leu Ala Thr Arg Tyr Gly Val Arg			
285	290	295	
gcc gcg cgt gcc tgc cac gag ggt cag ttc aac acc gtg gtc gcg ctc			1264
Ala Ala Arg Ala Cys His Glu Gly Gln Phe Asn Thr Val Val Ala Leu			
300	305	310	
aag ggg gag cgc atc cgg atg atc tcc ttc gat gag gcc gtg ggc acc			1312
Lys Gly Glu Arg Ile Arg Met Ile Ser Phe Asp Glu Ala Val Gly Thr			
315	320	325	
ctg aag aag gtg ccg atg gaa cgc tgg gtg acc gcc cag gct atg ttc			1360
Leu Lys Lys Val Pro Met Glu Arg Trp Val Thr Ala Gln Ala Met Phe			
330	335	340	345
ggt tagtcaggcc gcattcccgg ttccgcgccc gcggggccgg gttttttcat			1413
Gly			
gccccggaac acatcgggtat gaaatcgtga tatgcattac ttgacgggga agtgggggat			1473
ccgtcacctc gcgttgtcca actacagccc gcagcgccctg cgggaattct tccagcaatc			1533
cgccgattcc ccggcccgtc ccgtcgccgt ccaaccgcag tacaatctgc tggccccgcg			1593
ggattatgag accggtatcc gcccggtcgt ggacgagttc ggtcccgcgg			1643
<210> 10			
<211> 346			
<212> PRT			
<213> Corynebacterium thermoaminogenes			
<400> 10			
Met Gly Ala Met Arg Ile Ala Thr Leu Thr Ser Gly Gly Asp Cys Pro			
1	5	10	15
Gly Leu Asn Ala Val Ile Arg Gly Ile Val Arg Thr Ala Ser Asn Glu			
20	25	30	
Phe Gly Ser Thr Val Val Gly Tyr Gln Asp Gly Trp Glu Gly Leu Leu			
35	40	45	
Ala Asp Arg Arg Val Gln Leu Tyr Asp Asp Glu Asp Ile Asp Arg Ile			
50	55	60	

Leu Leu Arg Gly Gly Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp
65 70 75 80

Lys Phe Arg Ala Gly Ile Asp Gln Val Lys Ala Asn Leu Ala Asp Ala
85 90 95

Gly Ile Asp Ala Leu Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly
100 105 110

Ala Lys Trp Leu Ala Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys
115 120 125

Thr Ile Asp Asn Asp Val Asn Gly Thr Asp Phe Thr Phe Gly Phe Asp
130 135 140

Ser Ala Val Ser Val Ala Thr Asp Ala Ile Asp Arg Leu His Thr Thr
145 150 155 160

Ala Glu Ser His Asn Arg Val Met Ile Val Glu Val Met Gly Arg His
165 170 175

Val Gly Trp Ile Ala Leu His Ala Gly Met Ala Gly Gly Ala His Tyr
180 185 190

Thr Val Ile Pro Glu Val Pro Phe Asp Ile Ser Glu Ile Cys Lys Arg
195 200 205

Met Glu Arg Arg Phe Gln Met Gly Glu Lys Tyr Gly Ile Ile Val Val
210 215 220

Ala Glu Gly Ala Leu Pro Lys Glu Gly Thr Met Glu Leu Arg Glu Gly
225 230 235 240

Glu Val Asp Gln Phe Gly His Lys Thr Phe Thr Gly Ile Gly Gln Gln
245 250 255

Ile Ala Asp Glu Val His Arg Arg Leu Gly His Asp Val Arg Thr Thr
260 265 270

Val Leu Gly His Ile Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg
275 280 285

Val Leu Ala Thr Arg Tyr Gly Val Arg Ala Ala Arg Ala Cys His Glu
290 295 300

Gly Gln Phe Asn Thr Val Val Ala Leu Lys Gly Glu Arg Ile Arg Met
305 315 320

Ile Ser Phe Asp Glu Ala Val Gly Thr Leu Lys Lys Val Pro Met Glu
325 330 335

Arg Trp Val Thr Ala Gln Ala Met Phe Gly
340 345

<210> 11
<211> 498
<212> DNA
<213> Corynebacterium thermoaminogenes

<220>
<221> CDS
<222> (1)..(498)
<223>

<400> 11
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Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro Lys Arg Thr Gly
1 5 10 15
tgg gct cac acc acc acg ccg ttg acc gga ccg cag cga ttg cag tgg 96
Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln Arg Leu Gln Trp
20 25 30
acg cac ctg ccc gat gct ctt tac ccg gat gta tcc tat gac ctg gat 144
Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Val Ser Tyr Asp Leu Asp
35 40 45
gga tgc tat tcc ggc gga gcc gta ttt tct gac ggc acg ctt aaa ctt 192
Gly Cys Tyr Ser Gly Gly Ala Val Phe Ser Asp Gly Thr Leu Lys Leu
50 55 60
ttc tac acc ggc aac cga aaa att gac ggc aag cgc cgc gcc acc caa 240
Phe Tyr Thr Gly Asn Arg Lys Ile Asp Gly Lys Arg Arg Ala Thr Gln
65 70 75 80
aac ctc gtc gaa gtc gag gac cca act ggg ctg atg ggc ggc att cat 288
Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met Gly Gly Ile His
85 90 95
cgc cgc tcg cct aaa aat ccg ctt atc gac gga ccc gcc agc ggt ttt 336
Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro Ala Ser Gly Phe
100 105 110
acg ccc cac tac cgc gat ccc atg atc agc cct gat ggg gat ggt tgg 384
Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp Gly Asp Gly Trp
115 120 125
aag atg gtt ctt ggg gct cag cgc gaa aac ctc acc ggt gca gcg gtt 432
Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr Gly Ala Ala Val
130 135 140
cta tac cgc tcg gca gat ctt gaa aac tgg gaa ttc tcc ggt gaa atc 480
Leu Tyr Arg Ser Ala Asp Leu Glu Asn Trp Glu Phe Ser Gly Glu Ile

145 150 155 160

acc ttt gac ctc agc gac
Thr Phe Asp Leu Ser Asp
165

498

<210> 12
<211> 166
<212> PRT
<213> Corynebacterium thermoaminogenes

<400> 12

Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro Lys Arg Thr Gly
1 5 10 15

Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln Arg Leu Gln Trp
20 25 30

Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Val Ser Tyr Asp Leu Asp
35 40 45

Gly Cys Tyr Ser Gly Gly Ala Val Phe Ser Asp Gly Thr Leu Lys Leu
50 55 60

Phe Tyr Thr Gly Asn Arg Lys Ile Asp Gly Lys Arg Arg Ala Thr Gln
65 70 75 80

Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met Gly Gly Ile His
85 90 95

Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro Ala Ser Gly Phe
100 105 110

Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp Gly Asp Gly Trp
115 120 125

Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr Gly Ala Ala Val
130 135 140

Leu Tyr Arg Ser Ala Asp Leu Glu Asn Trp Glu Phe Ser Gly Glu Ile
145 150 155 160

Thr Phe Asp Leu Ser Asp
165

<210> 13
<211> 479
<212> DNA

<213> Corynebacterium thermoaminogenes

<220>

<221> CDS

<222> (1)..(477)

<223>

<400> 13

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Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro Lys Arg Thr Gly
1 5 10 15

tgg gct cac acc acc acg ccg ttg acc gga ccg cag cga ttg cag tgg 96
Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln Arg Leu Gln Trp
20 25 30

acg cac ctg ccc gac gct ctt tac ccg gat gca tcc tat gac ctg gat 144
Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Ala Ser Tyr Asp Leu Asp
35 40 45

gga tgc tat tcc ggt gga gcc gta ttt act gac ggc aca ctt aaa ctt 192
Gly Cys Tyr Ser Gly Gly Ala Val Phe Thr Asp Gly Thr Leu Lys Leu
50 55 60

ttc tac acc ggc aac cta aaa att gac ggc aag cgc cgc gcc acc caa 240
Phe Tyr Thr Gly Asn Leu Lys Ile Asp Gly Lys Arg Arg Ala Thr Gln
65 70 75 80

aac ctc gtc gaa gtc gag gac cca act ggg ctg atg ggc ggc att cat 288
Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met Gly Gly Ile His
85 90 95

cgc cgt tcg cct aaa aat ccg ctt atc gac gga ccc gcc agc ggt ttc 336
Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro Ala Ser Gly Phe
100 105 110

aca ccc cat tac cgc gat ccc atg atc agc cct gat ggt gat ggt tgg 384
Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp Gly Asp Gly Trp
115 120 125

aaa atg gtt ctt ggg gcc caa cgc gaa aac ctc acc ggt gca gcg gtt 432
Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr Gly Ala Ala Val
130 135 140

cta tac cgc tcg aca gat ctt gaa aac tgg gaa ttc tcc ggt gaa at 479
Leu Tyr Arg Ser Thr Asp Leu Glu Asn Trp Glu Phe Ser Gly Glu
145 150 155

<210> 14

<211> 159

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 14

Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro Lys Arg Thr Gly
1 5 10 15

Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln Arg Leu Gln Trp

20	25	30
Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Ala Ser Tyr Asp Leu Asp		
35	40	45
Gly Cys Tyr Ser Gly Gly Ala Val Phe Thr Asp Gly Thr Leu Lys Leu		
50	55	60
Phe Tyr Thr Gly Asn Leu Lys Ile Asp Gly Lys Arg Arg Ala Thr Gln		
65	70	75
Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met Gly Gly Ile His		
85	90	95
Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro Ala Ser Gly Phe		
100	105	110
Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp Gly Asp Gly Trp		
115	120	125
Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr Gly Ala Ala Val		
130	135	140
Leu Tyr Arg Ser Thr Asp Leu Glu Asn Trp Glu Phe Ser Gly Glu		
145	150	155

<210> 15
 <211> 490
 <212> DNA
 <213> Corynebacterium thermoaminogenes

<400> 15	
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aatgcattgg ggacacgcac gtagtaaaga tttagttcat tgggaaacat taccgattgc	120
tttagaacct ggagatgaag aagaaaaatg gttgtttctc tggtagaggt atagtcaaag	180
atgataagtt gtatttattt tatacagggtc accattatta taatgacgat gatcccgatc	240
atttttggca aaatcaaaat atggcttata gtgaagatgg cattcatttt caaaaatata	300
aacaaaaatgc aatcattcct accccacctg aagataatac acatcacttc agagatccaa	360
aggtatggga acatccatgg cttattatta catgatagta ggtagtcaaa atgatagaga	420
attaggacgt attatcttat atcgttctga ggatttatag aggggaattc tggctcctgag	480
atcaatccaa	490

<210> 16

gag gga acc atc gag atc gat gga aaa ctg ctt ccg gag gag ggc aag	846
Glu Gly Thr Ile Glu Ile Asp Gly Lys Leu Leu Pro Glu Glu Gly Lys	
55 60 65 70	
gac ctg gcc aag atc cgt gcc gac gtg ggc atg gtg ttc cag tct ttc	894
Asp Leu Ala Lys Ile Arg Ala Asp Val Gly Met Val Phe Gln Ser Phe	
75 80 85	
aac ctc ttc ccc cac ctc acc atc aag gac aat gtc acc ctc ggc ccg	942
Asn Leu Phe Pro His Leu Thr Ile Lys Asp Asn Val Thr Leu Gly Pro	
90 95 100	
atg aag gtc cgg aag atg aag aag tcc gag gcc aat gag gtg gcc atg	990
Met Lys Val Arg Lys Met Lys Lys Ser Glu Ala Asn Glu Val Ala Met	
105 110 115	
aag ctg ttg gaa cgc gtc ggc atc gcc aac cag gcc gag aaa tac ccg	1038
Lys Leu Leu Glu Arg Val Gly Ile Ala Asn Gln Ala Glu Lys Tyr Pro	
120 125 130	
gca cag ctc tcg ggc ggg cag cag cag cgc gtg gcc atc gcc cgc gca	1086
Ala Gln Leu Ser Gly Gly Gln Gln Gln Arg Val Ala Ile Ala Arg Ala	
135 140 145 150	
ctg gcg atg aac ccc aag atc atg ctt ttc gac gaa cca acc tcc gcc	1134
Leu Ala Met Asn Pro Lys Ile Met Leu Phe Asp Glu Pro Thr Ser Ala	
155 160 165	
ctc gac ccc gag atg gtc aac gag gtt ctg gac gtc atg gcg agt ctg	1182
Leu Asp Pro Glu Met Val Asn Glu Val Leu Asp Val Met Ala Ser Leu	
170 175 180	
gcc aag gaa ggc atg acc atg gtg tgt gtc acc cac gag atg ggt ttc	1230
Ala Lys Glu Gly Met Thr Met Val Cys Val Thr His Glu Met Gly Phe	
185 190 195	
gca cgc agg gcc gca gac cgt gtg ctg ttc atg tct gac ggc gcc atc	1278
Ala Arg Arg Ala Ala Asp Arg Val Leu Phe Met Ser Asp Gly Ala Ile	
200 205 210	
gtc gag gac tcc gac ccg gag acc ttc ttc acc aat cca caa acc gac	1326
Val Glu Asp Ser Asp Pro Glu Thr Phe Phe Thr Asn Pro Gln Thr Asp	
215 220 225 230	
cgg gcg aag gat ttc ctg ggc aag atc ctc gcc cac tgacctcccc	1372
Arg Ala Lys Asp Phe Leu Gly Lys Ile Leu Ala His	
235 240	
tcactctgtg tccaactccc ccgctggcca aaatcagcga ccatgaccaa caggagcatc	1432
a atg tcg cac aaa cgc atg ttc acc cgt ctc gcc gca gcc acc agc gca	1481
Met Ser His Lys Arg Met Phe Thr Arg Leu Ala Ala Ala Thr Ser Ala	
245 250 255	
gct gtt ctc gcc ggc atc acc ctc acc gcc tgt ggt gat tcc gag ggt	1529
Ala Val Leu Ala Gly Ile Thr Leu Thr Ala Cys Gly Asp Ser Glu Gly	
260 265 270	
ggt gac ggt ctg ctc gcc gcc atc gaa aat ggc aat gtc acc atc ggc	1577
Gly Asp Gly Leu Leu Ala Ala Ile Glu Asn Gly Asn Val Thr Ile Gly	
275 280 285 290	

acc aag tac gat cag ccg ggt ctg gga ctg cgt aac ccg gac aat tcc	1625
Thr Lys Tyr Asp Gln Pro Gly Leu Gly Leu Arg Asn Pro Asp Asn Ser	
295 300 305	
atg agc gga ctg gat gtc gac gtc gcg cag tac gtg gtc aac tcc atc	1673
Met Ser Gly Leu Asp Val Asp Val Ala Gln Tyr Val Val Asn Ser Ile	
310 315 320	
gcc gat gac aac ggt tgg gat cac ccc acc gtg gaa tgg cgc gag acc	1721
Ala Asp Asp Asn Gly Trp Asp His Pro Thr Val Glu Trp Arg Glu Thr	
325 330 335	
ccc tcc gcc cag cgc gag acc ctc atc cag aac ggt gag gtg gat atg	1769
Pro Ser Ala Gln Arg Glu Thr Leu Ile Gln Asn Gly Glu Val Asp Met	
340 345 350	
atc gcc gca acc tac tcc atc aac ccc gga cgc tcc gaa tcg gtg aac	1817
Ile Ala Ala Thr Tyr Ser Ile Asn Pro Gly Arg Ser Glu Ser Val Asn	
355 360 365 370	
ttc ggt gga cca tac ctc ctc acc cac cag gcc ctc ctg gtc cgc gag	1865
Phe Gly Gly Pro Tyr Leu Leu Thr His Gln Ala Leu Leu Val Arg Glu	
375 380 385	
gac gat gac cgc atc cag acc ctc gag gac ctc gat gac ggc ctg atc	1913
Asp Asp Asp Arg Ile Gln Thr Leu Glu Asp Leu Asp Asp Gly Leu Ile	
390 395 400	
ctg tgt tcc gtt acc gga tcc acc ccc gcc cag aag gtc aag gat gtc	1961
Leu Cys Ser Val Thr Gly Ser Thr Pro Ala Gln Lys Val Lys Asp Val	
405 410 415	
ctc ccc ggc gtc cag ctg cag gaa tac gac acc tac tcc tcc tgt gtg	2009
Leu Pro Gly Val Gln Leu Gln Glu Tyr Asp Thr Tyr Ser Ser Cys Val	
420 425 430	
gag gca ctg agc cag ggc aac gtc gat gca atg acc acc gac gcc acc	2057
Glu Ala Leu Ser Gln Gly Asn Val Asp Ala Met Thr Thr Asp Ala Thr	
435 440 445 450	
atc ctc ttc ggc tac gcg cag cag cgc gaa ggt gaa ttc cgc gtc gtg	2105
Ile Leu Phe Gly Tyr Ala Gln Gln Arg Glu Gly Glu Phe Arg Val Val	
455 460 465	
gag atg gaa cag gac ggc gag ccg ttc acc aat gag tac tac ggc atc	2153
Glu Met Glu Gln Asp Gly Glu Pro Phe Thr Asn Glu Tyr Tyr Gly Ile	
470 475 480	
ggg atc acc aag gat gac acc gaa gcc acc gat gcg atc aac gca gcg	2201
Gly Ile Thr Lys Asp Asp Thr Glu Ala Thr Asp Ala Ile Asn Ala Ala	
485 490 495	
ttg gag cgt atg tac gcc gac ggt tcc ttc cag cgt ttc ctc acc gag	2249
Leu Glu Arg Met Tyr Ala Asp Gly Ser Phe Gln Arg Phe Leu Thr Glu	
500 505 510	
aac ctc ggc gag gat tcc cag gtt gtc cag gag ggc acc ccg ggt gac	2297
Asn Leu Gly Glu Asp Ser Gln Val Val Gln Glu Gly Thr Pro Gly Asp	
515 520 525 530	

ctc tcc ttc ctg gac gag tgacctgacg gggccgaacg cccgatgagc 2345
 Leu Ser Phe Leu Asp Glu
 535

atgcgtggcc cccgcatccc ggggtgccac gcatcatcac tttcaccact gatcccctac 2405

cgttccttac cgaggagaaa ttcccc atg agt aca tta tgg gcg gat ctg ggt 2458
 Met Ser Thr Leu Trp Ala Asp Leu Gly
 540 545

ccg tca ctc cta ccc gca ttc tgg gtg aca atc caa ctc acc gtc tat 2506
 Pro Ser Leu Leu Pro Ala Phe Trp Val Thr Ile Gln Leu Thr Val Tyr
 550 555 560

tcc gcc atc gga tcc atg atc ctc ggt acc atc ctc acc gcc atg agg 2554
 Ser Ala Ile Gly Ser Met Ile Leu Gly Thr Ile Leu Thr Ala Met Arg
 565 570 575

gtg tcc ccg gtg aag atc ctg cgc agc ata tcc acc gcc tac atc aac 2602
 Val Ser Pro Val Lys Ile Leu Arg Ser Ile Ser Thr Ala Tyr Ile Asn
 580 585 590

acg gtc cgt aac acc cca ctg acc ctg gtg atc ctg ttc tgt tcc ttc 2650
 Thr Val Arg Asn Thr Pro Leu Thr Leu Val Ile Leu Phe Cys Ser Phe
 595 600 605

ggc ctg tat cag aat ctc ggt ctc acc ctc gcc ggt cgc gac agt tcc 2698
 Gly Leu Tyr Gln Asn Leu Gly Leu Thr Leu Ala Gly Arg Asp Ser Ser
 610 615 620 625

acc ttt ctg gcc gat aac aac ttc cgg ctc gcg gtg ctc gga ttc atc 2746
 Thr Phe Leu Ala Asp Asn Asn Phe Arg Leu Ala Val Leu Gly Phe Ile
 630 635 640

ctg tac acc tcc gcc ttc gtt gcg gaa tca ctc cgg tca ggc atc aac 2794
 Leu Tyr Thr Ser Ala Phe Val Ala Glu Ser Leu Arg Ser Gly Ile Asn
 645 650 655

acc gtg cac ttc ggg cag gcg gag gcc gcc cgg tcg ctg gga ctc ggt 2842
 Thr Val His Phe Gly Gln Ala Glu Ala Ala Arg Ser Leu Gly Leu Gly
 660 665 670

ttc agt gac atc ttc cgg tcc atc atc ttc ccc cag gcg gtg cgt gcc 2890
 Phe Ser Asp Ile Phe Arg Ser Ile Ile Phe Pro Gln Ala Val Arg Ala
 675 680 685

gcc atc atc ccg ctg ggc aac acc ctc atc gcc ctg acc aag aac acc 2938
 Ala Ile Ile Pro Leu Gly Asn Thr Leu Ile Ala Leu Thr Lys Asn Thr
 690 695 700 705

acg atc gcg tcc gtg atc ggc gtc ggt gag gcc tcg ctg ctg atg aag 2986
 Thr Ile Ala Ser Val Ile Gly Val Gly Glu Ala Ser Leu Leu Met Lys
 710 715 720

tcc acg att gaa aat cat gcc aac atg ctc ttc gtc gtg ttc gcc atc 3034
 Ser Thr Ile Glu Asn His Ala Asn Met Leu Phe Val Val Phe Ala Ile
 725 730 735

ttc gcc gtc ggc ttc atg atc ctc acc ctc ccc atg ggc ctg ggg ctt 3082
 Phe Ala Val Gly Phe Met Ile Leu Thr Leu Pro Met Gly Leu Gly Leu
 740 745 750

gga aaa ctc gct gag aaa atg gcg gtg aag aaa taatgtcctc ctccgtacgc	3135
Gly Lys Leu Ala Glu Lys Met Ala Val Lys Lys	
755 760	
gcaacagttc tctacgacgc ccccggtccc cggtggacgca ggtccaacac catcatcacc	3195
atcgccacca ccttggtggc agtggccgtc ctgttctgg gtg ggc agt gtt ctc	3249
Val Gly Ser Val Leu	
765	
cag gaa aac ggc cag ttg gac ggc gac aaa tgg acc ccg ttc ctc gat	3297
Gln Glu Asn Gly Gln Leu Asp Gly Asp Lys Trp Thr Pro Phe Leu Asp	
770 775 780 785	
ccc cag acc tgg acc acc tat ctt ctg ccc ggc ctg tgg gga acc ctg	3345
Pro Gln Thr Trp Thr Thr Tyr Leu Leu Pro Gly Leu Trp Gly Thr Leu	
790 795 800	
aag gca gcg gtg gcc tcc atc ctt ctc gcg ctg atc atg ggc acc ctg	3393
Lys Ala Ala Val Ala Ser Ile Leu Leu Ala Leu Ile Met Gly Thr Leu	
805 810 815	
ctc ggg ctc gga cgc atc tcc gaa atc cgg ctc ctg cgc tgg ttc tgc	3441
Leu Gly Leu Gly Arg Ile Ser Glu Ile Arg Leu Leu Arg Trp Phe Cys	
820 825 830	
ggg atc atc atc gag acc ttc cgt gcc atc ccg gtg ctg atc ctc atg	3489
Gly Ile Ile Ile Glu Thr Phe Arg Ala Ile Pro Val Leu Ile Leu Met	
835 840 845	
atc ttc gcc tat cag ttg ttc gcc cgt tac cag ctc gtt cca tca cgc	3537
Ile Phe Ala Tyr Gln Leu Phe Ala Arg Tyr Gln Leu Val Pro Ser Arg	
850 855 860 865	
cag ctg gcc ttc gcc gcg gtg gtc ttc ggt ctc acc atg tac aac ggc	3585
Gln Leu Ala Phe Ala Ala Val Val Phe Gly Leu Thr Met Tyr Asn Gly	
870 875 880	
tcc gtc atc gcc gag atc ctt aga tgc ggt atc gcc tcc ctg ccg aag	3633
Ser Val Ile Ala Glu Ile Leu Arg Ser Gly Ile Ala Ser Leu Pro Lys	
885 890 895	
gga cag cgt gag gcg gcg atc gcc ctg ggc atg tca acc cgc cag acc	3681
Gly Gln Arg Glu Ala Ala Ile Ala Leu Gly Met Ser Thr Arg Gln Thr	
900 905 910	
acc tgg tgc atc ctg ctc ccc cag gcg gtg gca gcg atg ctg ccc gcc	3729
Thr Trp Ser Ile Leu Leu Pro Gln Ala Val Ala Ala Met Leu Pro Ala	
915 920 925	
ctg atc gcg cag atg gtc atc gcg ctg aag gac tcc gcc ctc ggt tac	3777
Leu Ile Ala Gln Met Val Ile Ala Leu Lys Asp Ser Ala Leu Gly Tyr	
930 935 940 945	
cag atc ggt tat atc gag gtg gta cgc tcc ggt atc cag tcc gca tcc	3825
Gln Ile Gly Tyr Ile Glu Val Val Arg Ser Gly Ile Gln Ser Ala Ser	
950 955 960	
gtc aac cgg aac tac ctg gct gcc ctc gcg gtg gtc gcg gtc atc atg	3873
Val Asn Arg Asn Tyr Leu Ala Ala Leu Ala Val Val Ala Val Ile Met	

965 970 975
 atc ctg atc aac ttc gca ctg acc gca ctg gca gag cgt atc cag cgt 3921
 Ile Leu Ile Asn Phe Ala Leu Thr Ala Leu Ala Glu Arg Ile Gln Arg
 980 985 990
 cag ctg cgt gcc gga cgt gcc cgc agg aac att gtg gca aag gtg ccc 3969
 Gln Leu Arg Ala Gly Arg Ala Arg Arg Asn Ile Val Ala Lys Val Pro
 995 1000 1005
 gag gaa ccc gat cag ggc ctg gat acc aag gac aat gtg aac gtg 4014
 Glu Glu Pro Asp Gln Gly Leu Asp Thr Lys Asp Asn Val Asn Val
 1010 1015 1020
 gat tgg cac gat ccc gat tac aag gaa gtc aaa cac ccg gga ccg 4059
 Asp Trp His Asp Pro Asp Tyr Lys Glu Val Lys His Pro Gly Pro
 1025 1030 1035
 tca ttc tgacaggtcc ctggatcccc gctgcggtca ggaggcgggt gcaacaatga 4115
 Ser Phe
 1040
 agtccggctg cccagatgtc tggggcagcc ggactttgtg gcagatcaat gctgactgag 4175
 gtccctcgatg cgctcatcga gagcctcccg ggccaggtcc atcgacatac ccgcggggaa 4235
 tccacgacgg gcaagtgtc 4254

 <210> 17
 <211> 242
 <212> PRT
 <213> Corynebacterium thermoaminogenes

 <400> 17

 Met Ile Lys Met Thr Gly Val Gln Lys Phe Phe Asp Asp Phe Gln Ala
 1 5 10 15

 Leu Thr Asp Ile Asn Leu Glu Val Pro Ala Gly Gln Val Val Val Val
 20 25 30

 Leu Gly Pro Ser Gly Ser Gly Lys Ser Thr Leu Cys Arg Thr Ile Asn
 35 40 45

 Arg Leu Glu Thr Ile Glu Glu Gly Thr Ile Glu Ile Asp Gly Lys Leu
 50 55 60

 Leu Pro Glu Glu Gly Lys Asp Leu Ala Lys Ile Arg Ala Asp Val Gly
 65 70 75 80

 Met Val Phe Gln Ser Phe Asn Leu Phe Pro His Leu Thr Ile Lys Asp
 85 90 95

 Asn Val Thr Leu Gly Pro Met Lys Val Arg Lys Met Lys Lys Ser Glu

100	105	110
Ala Asn Glu Val Ala Met Lys Leu Leu Glu Arg Val Gly Ile Ala Asn		
115	120	125
Gln Ala Glu Lys Tyr Pro Ala Gln Leu Ser Gly Gly Gln Gln Gln Arg		
130	135	140
Val Ala Ile Ala Arg Ala Leu Ala Met Asn Pro Lys Ile Met Leu Phe		
145	150	155 160
Asp Glu Pro Thr Ser Ala Leu Asp Pro Glu Met Val Asn Glu Val Leu		
165	170	175
Asp Val Met Ala Ser Leu Ala Lys Glu Gly Met Thr Met Val Cys Val		
180	185	190
Thr His Glu Met Gly Phe Ala Arg Arg Ala Ala Asp Arg Val Leu Phe		
195	200	205
Met Ser Asp Gly Ala Ile Val Glu Asp Ser Asp Pro Glu Thr Phe Phe		
210	215	220
Thr Asn Pro Gln Thr Asp Arg Ala Lys Asp Phe Leu Gly Lys Ile Leu		
225	230	235 240

Ala His

<210> 18
 <211> 294
 <212> PRT
 <213> Corynebacterium thermoaminogenes

<400> 18

Met Ser His Lys Arg Met Phe Thr Arg Leu Ala Ala Ala Thr Ser Ala		
1	5	10 15
Ala Val Leu Ala Gly Ile Thr Leu Thr Ala Cys Gly Asp Ser Glu Gly		
20	25	30
Gly Asp Gly Leu Leu Ala Ala Ile Glu Asn Gly Asn Val Thr Ile Gly		
35	40	45
Thr Lys Tyr Asp Gln Pro Gly Leu Gly Leu Arg Asn Pro Asp Asn Ser		
50	55	60

Met Ser Gly Leu Asp Val Asp Val Ala Gln Tyr Val Val Asn Ser Ile
65 70 75 80

Ala Asp Asp Asn Gly Trp Asp His Pro Thr Val Glu Trp Arg Glu Thr
85 90 95

Pro Ser Ala Gln Arg Glu Thr Leu Ile Gln Asn Gly Glu Val Asp Met
100 105 110

Ile Ala Ala Thr Tyr Ser Ile Asn Pro Gly Arg Ser Glu Ser Val Asn
115 120 125

Phe Gly Gly Pro Tyr Leu Leu Thr His Gln Ala Leu Leu Val Arg Glu
130 135 140

Asp Asp Asp Arg Ile Gln Thr Leu Glu Asp Leu Asp Asp Gly Leu Ile
145 150 155 160

Leu Cys Ser Val Thr Gly Ser Thr Pro Ala Gln Lys Val Lys Asp Val
165 170 175

Leu Pro Gly Val Gln Leu Gln Glu Tyr Asp Thr Tyr Ser Ser Cys Val
180 185 190

Glu Ala Leu Ser Gln Gly Asn Val Asp Ala Met Thr Thr Asp Ala Thr
195 200 205

Ile Leu Phe Gly Tyr Ala Gln Gln Arg Glu Gly Glu Phe Arg Val Val
210 215 220

Glu Met Glu Gln Asp Gly Glu Pro Phe Thr Asn Glu Tyr Tyr Gly Ile
225 230 235 240

Gly Ile Thr Lys Asp Asp Thr Glu Ala Thr Asp Ala Ile Asn Ala Ala
245 250 255

Leu Glu Arg Met Tyr Ala Asp Gly Ser Phe Gln Arg Phe Leu Thr Glu
260 265 270

Asn Leu Gly Glu Asp Ser Gln Val Val Gln Glu Gly Thr Pro Gly Asp
275 280 285

Leu Ser Phe Leu Asp Glu
290

<210> 19
 <211> 228
 <212> PRT
 <213> Corynebacterium thermoaminogenes

<400> 19

Met Ser Thr Leu Trp Ala Asp Leu Gly Pro Ser Leu Leu Pro Ala Phe
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Trp Val Thr Ile Gln Leu Thr Val Tyr Ser Ala Ile Gly Ser Met Ile
 20 25 30

Leu Gly Thr Ile Leu Thr Ala Met Arg Val Ser Pro Val Lys Ile Leu
 35 40 45

Arg Ser Ile Ser Thr Ala Tyr Ile Asn Thr Val Arg Asn Thr Pro Leu
 50 55 60

Thr Leu Val Ile Leu Phe Cys Ser Phe Gly Leu Tyr Gln Asn Leu Gly
 65 70 75 80

Leu Thr Leu Ala Gly Arg Asp Ser Ser Thr Phe Leu Ala Asp Asn Asn
 85 90 95

Phe Arg Leu Ala Val Leu Gly Phe Ile Leu Tyr Thr Ser Ala Phe Val
 100 105 110

Ala Glu Ser Leu Arg Ser Gly Ile Asn Thr Val His Phe Gly Gln Ala
 115 120 125

Glu Ala Ala Arg Ser Leu Gly Leu Gly Phe Ser Asp Ile Phe Arg Ser
 130 135 140

Ile Ile Phe Pro Gln Ala Val Arg Ala Ala Ile Ile Pro Leu Gly Asn
 145 150 155 160

Thr Leu Ile Ala Leu Thr Lys Asn Thr Thr Ile Ala Ser Val Ile Gly
 165 170 175

Val Gly Glu Ala Ser Leu Leu Met Lys Ser Thr Ile Glu Asn His Ala
 180 185 190

Asn Met Leu Phe Val Val Phe Ala Ile Phe Ala Val Gly Phe Met Ile
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Leu Thr Leu Pro Met Gly Leu Gly Leu Gly Lys Leu Ala Glu Lys Met
 210 215 220

Ala Val Lys Lys
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<210> 20
<211> 277
<212> PRT
<213> Corynebacterium thermoaminogenes

<400> 20

Val Gly Ser Val Leu Gln Glu Asn Gly Gln Leu Asp Gly Asp Lys Trp
1 5 10 15

Thr Pro Phe Leu Asp Pro Gln Thr Trp Thr Thr Tyr Leu Leu Pro Gly
20 25 30

Leu Trp Gly Thr Leu Lys Ala Ala Val Ala Ser Ile Leu Leu Ala Leu
35 40 45

Ile Met Gly Thr Leu Leu Gly Leu Gly Arg Ile Ser Glu Ile Arg Leu
50 55 60

Leu Arg Trp Phe Cys Gly Ile Ile Ile Glu Thr Phe Arg Ala Ile Pro
65 70 75 80

Val Leu Ile Leu Met Ile Phe Ala Tyr Gln Leu Phe Ala Arg Tyr Gln
85 90 95

Leu Val Pro Ser Arg Gln Leu Ala Phe Ala Ala Val Val Phe Gly Leu
100 105 110

Thr Met Tyr Asn Gly Ser Val Ile Ala Glu Ile Leu Arg Ser Gly Ile
115 120 125

Ala Ser Leu Pro Lys Gly Gln Arg Glu Ala Ala Ile Ala Leu Gly Met
130 135 140

Ser Thr Arg Gln Thr Thr Trp Ser Ile Leu Leu Pro Gln Ala Val Ala
145 150 155 160

Ala Met Leu Pro Ala Leu Ile Ala Gln Met Val Ile Ala Leu Lys Asp
165 170 175

Ser Ala Leu Gly Tyr Gln Ile Gly Tyr Ile Glu Val Val Arg Ser Gly
180 185 190

Ile Gln Ser Ala Ser Val Asn Arg Asn Tyr Leu Ala Ala Leu Ala Val
 195 200 205

Val Ala Val Ile Met Ile Leu Ile Asn Phe Ala Leu Thr Ala Leu Ala
 210 215 220

Glu Arg Ile Gln Arg Gln Leu Arg Ala Gly Arg Ala Arg Arg Asn Ile
 225 230 235 240

Val Ala Lys Val Pro Glu Glu Pro Asp Gln Gly Leu Asp Thr Lys Asp
 245 250 255

Asn Val Asn Val Asp Trp His Asp Pro Asp Tyr Lys Glu Val Lys His
 260 265 270

Pro Gly Pro Ser Phe
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<210> 21
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 <212> DNA
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 tccataatgt ggctgtaac acccttgggc tcaaggcttc cacgccccac cgggaccctc 180
 atcagcaggt gaaacagacc ctcttgcaat gctttgttaa aaagaaccgc cctttgtgcy 240
 tacccttggt tcaattgtgc ggcactgcc accagctttc ctcaggattg aacacgggtc 300
 ggaaatcctc cccggatacc ctgcacgccc cacctcccac accgacaccg gcggggaggg 360
 ccgggcacgt ttccagctgc ggggtgatgga agcgggtgcc ggtcccccg tgcataaac 420
 gaaatgaaaa acattccaac aggaggtgtg gaa atg gcc gat caa gca aaa ctt 474
 Met Ala Asp Gln Ala Lys Leu
 1 5
 ggt ggc aaa ccc aca gat gac acc aac ttc gcg atg atc cgt gat ggc 522
 Gly Gly Lys Pro Thr Asp Asp Thr Asn Phe Ala Met Ile Arg Asp Gly
 10 15 20
 gtt gca tct tat ttg aac gac tcc gac ccg gag gag acc aag gag tgg 570
 Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Lys Glu Trp
 25 30 35

atg gac tcc cta gac ggt cta ctg cag gat tcc tct ccg gag cgc gcc Met Asp Ser Leu Asp Gly Leu Leu Gln Asp Ser Ser Pro Glu Arg Ala 40 45 50 55	618
cgt tac ctg atg ctg cgc ctg ctg gag cgg gca tcc gcc aag cgt gtc Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys Arg Val 60 65 70	666
cca ctg ccc ccg atg acg tcc acc gat tac gtc aac acc atc ccc aca Pro Leu Pro Pro Met Thr Ser Thr Asp Tyr Val Asn Thr Ile Pro Thr 75 80 85	714
tcc atg gag ccc gat ttc ccg ggt gat gag gag atg gag aag cgc tac Ser Met Glu Pro Asp Phe Pro Gly Asp Glu Glu Met Glu Lys Arg Tyr 90 95 100	762
cgc cgc tgg atg cgc tgg aac gcc gcc atc atg gtg cac cgt gcc cag Arg Arg Trp Met Arg Trp Asn Ala Ala Ile Met Val His Arg Ala Gln 105 110 115	810
cgc ccg gga atc ggt gtg ggt ggg cac atc tcc acc tac gcc ggc gcc Arg Pro Gly Ile Gly Val Gly Gly His Ile Ser Thr Tyr Ala Gly Ala 120 125 130 135	858
gcc cca ctc tac gag gtc ggt ttc aac cac ttc ttc cgc ggc aag gac Ala Pro Leu Tyr Glu Val Gly Phe Asn His Phe Phe Arg Gly Lys Asp 140 145 150	906
cac ccg ggt ggc ggt gac cag gtc ttc ttc cag ggt cac gcc tcc ccg His Pro Gly Gly Gly Asp Gln Val Phe Phe Gln Gly His Ala Ser Pro 155 160 165	954
ggc atg tac gcc cgc gcc ttc ctc gag ggc cgt ctc acc gag agc gat Gly Met Tyr Ala Arg Ala Phe Leu Glu Gly Arg Leu Thr Glu Ser Asp 170 175 180	1002
ctg gac agc ttc cgc cag gag gtc tcc tac gaa ggt ggt ggc atc ccg Leu Asp Ser Phe Arg Gln Glu Val Ser Tyr Glu Gly Gly Gly Ile Pro 185 190 195	1050
tcc tac ccg cac ccg cac ggc atg ccg gac ttc tgg gag ttc ccg acc Ser Tyr Pro His Pro His Gly Met Pro Asp Phe Trp Glu Phe Pro Thr 200 205 210 215	1098
gtg tcc atg ggc ctc ggg ccc atg gat gcc atc tac cag gcg cgc ttc Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg Phe 220 225 230	1146
aac cgc tac ctg cac aac cgt ggc atc aag gac acc tcg gag cag cac Asn Arg Tyr Leu His Asn Arg Gly Ile Lys Asp Thr Ser Glu Gln His 235 240 245	1194
gtc tgg gca ttc ctc ggt gac ggc gag atg gat gag ccg gag tcc cgt Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser Arg 250 255 260	1242
ggt ctc atc cac cag gct gcg ctg aac aac ctg gac aac ctc acc ttc Gly Leu Ile His Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr Phe 265 270 275	1290
gtg atc aac tgc aac ctg cag cgt ctt gat ggc ccg gtc cgc ggt aac	1338

Val Ile Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Arg Gly Asn	
280 285 290 295	
acc aag atc atc cag gaa ctc gag tcc ttc ttc cgt ggt gcc ggc tgg	1386
Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly Trp	
300 305 310	
tcc gtc atc aag gtc atc tgg ggc cgt gag tgg gat gaa ctg ctg gag	1434
Ser Val Ile Lys Val Ile Trp Gly Arg Glu Trp Asp Glu Leu Leu Glu	
315 320 325	
aag gac cag gac ggt gct ctt gtc gag gtc atg aac aac acc tcc gac	1482
Lys Asp Gln Asp Gly Ala Leu Val Glu Val Met Asn Asn Thr Ser Asp	
330 335 340	
ggt gac tac cag acc ttc aag gcc aat gac ggt gcc tac gtc cgt gag	1530
Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg Glu	
345 350 355	
cac ttc ttc ggc cgt gac ccc cgc acc ctc aag ctc gtc gag gac atg	1578
His Phe Phe Gly Arg Asp Pro Arg Thr Leu Lys Leu Val Glu Asp Met	
360 365 370 375	
acc gac gag gag atc tgg aag ctg ccc cgt ggt ggc cat gac tac cgt	1626
Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr Arg	
380 385 390	
aag gtc tac gcc gcc tac aag cgt gcg ctg gag acc aag gac cgc ccg	1674
Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg Pro	
395 400 405	
acc gtc att ctc gcc cat acc atc aag ggc tac ggc ctg ggc cac aac	1722
Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His Asn	
410 415 420	
ttc gag ggc cgc aac gcg acc cac cag atg aag aag ctg acc ctg gat	1770
Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu Asp	
425 430 435	
gac ctg aag ctg ttc cgt gac aag cag ggt ctg ccc atc acc gat gag	1818
Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Leu Pro Ile Thr Asp Glu	
440 445 450 455	
gag ctg gag aag gat ccc tac ctg cct ccg tac tac cac ccg ggt gag	1866
Glu Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly Glu	
460 465 470	
gac gca ccg gag atc aag tac atg aag gag cgt cgc cag gcg ctc ggt	1914
Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Gln Ala Leu Gly	
475 480 485	
ggt ttc ctg ccg gag cgc cgt gag aag tac gag cca ctg cag gtt ccc	1962
Gly Phe Leu Pro Glu Arg Arg Glu Lys Tyr Glu Pro Leu Gln Val Pro	
490 495 500	
ccg ctg gac aag ctg ccg tcc gtg cgc aag ggt tcc ggc aag cag cag	2010
Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln Gln	
505 510 515	
gtg gcc acc acc atg gcc acg gtg cgt acc ttc aag gaa ctc atg cgg	2058
Val Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met Arg	

520	525	530	535		
gac aag aac ctg gcc gac cgc ttg gtc ccg atc atc ccg gat gag gcc Asp Lys Asn Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu Ala	540	545	550	2106	
cgc acc ttc ggc ctg gac tcc tgg ttc ccg acc ctg aaa atc tac aac Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr Asn	555	560	565	2154	
ccg cac ggt cag aac tac gtg ccg gtc gac cat gac ctc atg ctg tcc Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu Ser	570	575	580	2202	
tac cgt gag gcc aag gac ggc cag atc ctg cat gag ggc atc aac gag Tyr Arg Glu Ala Lys Asp Gly Gln Ile Leu His Glu Gly Ile Asn Glu	585	590	595	2250	
gcc ggt tcc gtg gca tcg ttt atc gcc gcc gga acc tcc tac gcc acc Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr Ser Tyr Ala Thr	600	605	610	615	2298
cat ggc gag gcc atg atc ccg ctg tac atc ttc tac tcg atg ttc ggc His Gly Glu Ala Met Ile Pro Leu Tyr Ile Phe Tyr Ser Met Phe Gly	620	625	630	2346	
ttc cag cgc acc ggt gac ggc atc tgg gcc gca gcc gac cag atg acg Phe Gln Arg Thr Gly Asp Gly Ile Trp Ala Ala Ala Asp Gln Met Thr	635	640	645	2394	
cgt ggt ttc ctc ctg ggc gcc acc gcc ggt cgc acc acc ctg acc ggt Arg Gly Phe Leu Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly	650	655	660	2442	
gag ggc ctc cag cac atg gat ggc cac tcc ccg atc ctg gcc tcc acc Glu Gly Leu Gln His Met Asp Gly His Ser Pro Ile Leu Ala Ser Thr	665	670	675	2490	
aac ccc ggt gtg gag acc tat gac ccg gcg ttc tcc tac gag atc gcg Asn Pro Gly Val Glu Thr Tyr Asp Pro Ala Phe Ser Tyr Glu Ile Ala	680	685	690	695	2538
cac ctg gtc cac cgc ggc atc gac cgc atg tac gga ccg ggc aag ggt His Leu Val His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly Lys Gly	700	705	710	2586	
gag aat gtc atc tac tac ctc acc atc tac aac gag cca acc ccg cag Glu Asn Val Ile Tyr Tyr Leu Thr Ile Tyr Asn Glu Pro Thr Pro Gln	715	720	725	2634	
ccg gct gag cct gag gat ctg gac gtc gag ggc ctg cac aag ggc atc Pro Ala Glu Pro Glu Asp Leu Asp Val Glu Gly Leu His Lys Gly Ile	730	735	740	2682	
tac ctc tac gac aag gcc gcc gag ggt gag ggc cat gag gcc tcg atc Tyr Leu Tyr Asp Lys Ala Ala Glu Gly Glu Gly His Glu Ala Ser Ile	745	750	755	2730	
ctg gcc tcc ggc atc ggc atg cag tgg gca ctg cgc gcc cgt gac atc Leu Ala Ser Gly Ile Gly Met Gln Trp Ala Leu Arg Ala Arg Asp Ile	760	765	770	775	2778

ctc gcc gag gat tac ggc atc cgt gcc aac atc ttc tcc gcc acc tcg Leu Ala Glu Asp Tyr Gly Ile Arg Ala Asn Ile Phe Ser Ala Thr Ser 780 785 790	2826
tgg gtg gag ctg gcc cgc gac ggt gcc cgc cgt aac ctg gag gcg ctg Trp Val Glu Leu Ala Arg Asp Gly Ala Arg Arg Asn Leu Glu Ala Leu 795 800 805	2874
cgc aac ccg ggt gcg gat gtc ggt gag gca ttc gtg acc acc cag ctg Arg Asn Pro Gly Ala Asp Val Gly Glu Ala Phe Val Thr Thr Gln Leu 810 815 820	2922
aag aag ggt tcc ggc ccc tac gtc gcg gtg tcc gac ttc gcg acc gac Lys Lys Gly Ser Gly Pro Tyr Val Ala Val Ser Asp Phe Ala Thr Asp 825 830 835	2970
ctg ccg aac cag atc cgc gag tgg gtt ccc ggt gac tac atc gtc ctc Leu Pro Asn Gln Ile Arg Glu Trp Val Pro Gly Asp Tyr Ile Val Leu 840 845 850 855	3018
ggt gcc gac ggc ttc ggt ttc tcc gat acc cgt ccg gca gcc cgt cgt Gly Ala Asp Gly Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg Arg 860 865 870	3066
tac ttc aac atc gac gcc gag tcc atc gtc gtg gcg gtc ctg cgc ggc Tyr Phe Asn Ile Asp Ala Glu Ser Ile Val Val Ala Val Leu Arg Gly 875 880 885	3114
ctg gtc cgc gag ggt gtc atc gat gcc tcc gtg gcg gcg cac gcg gct Leu Val Arg Glu Gly Val Ile Asp Ala Ser Val Ala Ala His Ala Ala 890 895 900	3162
gag aag tac aag ctg tcc gac ccg acg gca cca cag gtc gat ccg gac Glu Lys Tyr Lys Leu Ser Asp Pro Thr Ala Pro Gln Val Asp Pro Asp 905 910 915	3210
gca ccg atc gag tagacctgct tgctcgacgaa aaacaccccc gccccctcac Ala Pro Ile Glu 920	3262
atgatgaggg gggcgggggt gtgctcgttt acggcgggta caggggggta tcagcccagc	3322
atcgcccttat cggagagcgt cgcgcacctg atcttggcga attcctgcag cagatcccgc	3382
acggtgagct tctgcttcac ctctgcgctg gcctcataga cgatccgtcc ctcgtgcac	3442
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Met Ala Asp Gln Ala Lys Leu Gly Gly Lys Pro Thr Asp Asp Thr Asn
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Phe Ala Met Ile Arg Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp
 20 25 30

Pro Glu Glu Thr Lys Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln
 35 40 45

Asp Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu
 50 55 60

Arg Ala Ser Ala Lys Arg Val Pro Leu Pro Pro Met Thr Ser Thr Asp
 65 70 75 80

Tyr Val Asn Thr Ile Pro Thr Ser Met Glu Pro Asp Phe Pro Gly Asp
 85 90 95

Glu Glu Met Glu Lys Arg Tyr Arg Arg Trp Met Arg Trp Asn Ala Ala
 100 105 110

Ile Met Val His Arg Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His
 115 120 125

Ile Ser Thr Tyr Ala Gly Ala Ala Pro Leu Tyr Glu Val Gly Phe Asn
 130 135 140

His Phe Phe Arg Gly Lys Asp His Pro Gly Gly Gly Asp Gln Val Phe
 145 150 155 160

Phe Gln Gly His Ala Ser Pro Gly Met Tyr Ala Arg Ala Phe Leu Glu
 165 170 175

Gly Arg Leu Thr Glu Ser Asp Leu Asp Ser Phe Arg Gln Glu Val Ser
 180 185 190

Tyr Glu Gly Gly Gly Ile Pro Ser Tyr Pro His Pro His Gly Met Pro
 195 200 205

Asp Phe Trp Glu Phe Pro Thr Val Ser Met Gly Leu Gly Pro Met Asp
 210 215 220

Ala Ile Tyr Gln Ala Arg Phe Asn Arg Tyr Leu His Asn Arg Gly Ile
 225 230 235 240

Lys Asp Thr Ser Glu Gln His Val Trp Ala Phe Leu Gly Asp Gly Glu

245	250	255
Met Asp Glu Pro Glu Ser Arg Gly Leu Ile His Gln Ala Ala Leu Asn		
260	265	270
Asn Leu Asp Asn Leu Thr Phe Val Ile Asn Cys Asn Leu Gln Arg Leu		
275	280	285
Asp Gly Pro Val Arg Gly Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser		
290	295	300
Phe Phe Arg Gly Ala Gly Trp Ser Val Ile Lys Val Ile Trp Gly Arg		
305	310	315
Glu Trp Asp Glu Leu Leu Glu Lys Asp Gln Asp Gly Ala Leu Val Glu		
325	330	335
Val Met Asn Asn Thr Ser Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn		
340	345	350
Asp Gly Ala Tyr Val Arg Glu His Phe Phe Gly Arg Asp Pro Arg Thr		
355	360	365
Leu Lys Leu Val Glu Asp Met Thr Asp Glu Glu Ile Trp Lys Leu Pro		
370	375	380
Arg Gly Gly His Asp Tyr Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala		
385	390	395
Leu Glu Thr Lys Asp Arg Pro Thr Val Ile Leu Ala His Thr Ile Lys		
405	410	415
Gly Tyr Gly Leu Gly His Asn Phe Glu Gly Arg Asn Ala Thr His Gln		
420	425	430
Met Lys Lys Leu Thr Leu Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln		
435	440	445
Gly Leu Pro Ile Thr Asp Glu Glu Leu Glu Lys Asp Pro Tyr Leu Pro		
450	455	460
Pro Tyr Tyr His Pro Gly Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys		
465	470	475
Glu Arg Arg Gln Ala Leu Gly Gly Phe Leu Pro Glu Arg Arg Glu Lys		
485	490	495

Tyr Glu Pro Leu Gln Val Pro Pro Leu Asp Lys Leu Arg Ser Val Arg
 500 505 510

Lys Gly Ser Gly Lys Gln Gln Val Ala Thr Thr Met Ala Thr Val Arg
 515 520 525

Thr Phe Lys Glu Leu Met Arg Asp Lys Asn Leu Ala Asp Arg Leu Val
 530 535 540

Pro Ile Ile Pro Asp Glu Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe
 545 550 555 560

Pro Thr Leu Lys Ile Tyr Asn Pro His Gly Gln Asn Tyr Val Pro Val
 565 570 575

Asp His Asp Leu Met Leu Ser Tyr Arg Glu Ala Lys Asp Gly Gln Ile
 580 585 590

Leu His Glu Gly Ile Asn Glu Ala Gly Ser Val Ala Ser Phe Ile Ala
 595 600 605

Ala Gly Thr Ser Tyr Ala Thr His Gly Glu Ala Met Ile Pro Leu Tyr
 610 615 620

Ile Phe Tyr Ser Met Phe Gly Phe Gln Arg Thr Gly Asp Gly Ile Trp
 625 630 635 640

Ala Ala Ala Asp Gln Met Thr Arg Gly Phe Leu Leu Gly Ala Thr Ala
 645 650 655

Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln His Met Asp Gly His
 660 665 670

Ser Pro Ile Leu Ala Ser Thr Asn Pro Gly Val Glu Thr Tyr Asp Pro
 675 680 685

Ala Phe Ser Tyr Glu Ile Ala His Leu Val His Arg Gly Ile Asp Arg
 690 695 700

Met Tyr Gly Pro Gly Lys Gly Glu Asn Val Ile Tyr Tyr Leu Thr Ile
 705 710 715 720

Tyr Asn Glu Pro Thr Pro Gln Pro Ala Glu Pro Glu Asp Leu Asp Val
 725 730 735

Glu Gly Leu His Lys Gly Ile Tyr Leu Tyr Asp Lys Ala Ala Glu Gly
740 745 750

Glu Gly His Glu Ala Ser Ile Leu Ala Ser Gly Ile Gly Met Gln Trp
755 760 765

Ala Leu Arg Ala Arg Asp Ile Leu Ala Glu Asp Tyr Gly Ile Arg Ala
770 775 780

Asn Ile Phe Ser Ala Thr Ser Trp Val Glu Leu Ala Arg Asp Gly Ala
785 790 795 800

Arg Arg Asn Leu Glu Ala Leu Arg Asn Pro Gly Ala Asp Val Gly Glu
805 810 815

Ala Phe Val Thr Thr Gln Leu Lys Lys Gly Ser Gly Pro Tyr Val Ala
820 825 830

Val Ser Asp Phe Ala Thr Asp Leu Pro Asn Gln Ile Arg Glu Trp Val
835 840 845

Pro Gly Asp Tyr Ile Val Leu Gly Ala Asp Gly Phe Gly Phe Ser Asp
850 855 860

Thr Arg Pro Ala Ala Arg Arg Tyr Phe Asn Ile Asp Ala Glu Ser Ile
865 870 875 880

Val Val Ala Val Leu Arg Gly Leu Val Arg Glu Gly Val Ile Asp Ala
885 890 895

Ser Val Ala Ala His Ala Ala Glu Lys Tyr Lys Leu Ser Asp Pro Thr
900 905 910

Ala Pro Gln Val Asp Pro Asp Ala Pro Ile Glu
915 920

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<211> 4012
<212> DNA
<213> Corynebacterium thermoaminogenes

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<222> (319) .. (3735)
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<400> 23
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ggcaatgggg gtctcgggcg gggggcattc ttttcacggc aaggtggtga aattccgcag	180
gtcactcccc ggccggcggt agagaacgga gcgaaaacgg aaagcaatac gtgggttttcc	240
ggactggccg ttacgatgtt ctgaagagtg actgccatca cccaacaggc tggctctcgt	300
cgaaaggaac aaaaactg tgg tta caa caa cac cct cca cgc tgc cgg cgt	351
Trp Leu Gln Gln His Pro Pro Arg Cys Arg Arg	
1 5 10	
tca aaa aga tcc tgg tgg cca acc gag gtg aaa tcg cgg tgc gag cat	399
Ser Lys Arg Ser Trp Trp Pro Thr Glu Val Lys Ser Arg Cys Glu His	
15 20 25	
tcc gcg ccg cct acg aga ccg ggg ccg caa ccg tgg cca tct acc ccc	447
Ser Ala Pro Pro Thr Arg Pro Gly Pro Gln Pro Trp Pro Ser Thr Pro	
30 35 40	
ggg agg acc gtg gct cct tcc acc gct cct tcg cct ccg agg cgg tga	495
Gly Arg Thr Val Ala Pro Ser Thr Ala Pro Ser Pro Pro Arg Arg	
45 50 55	
gga tcg gaa ccg agg gct cac ccg tca agg cgt acc tcg ata ttg atg	543
Gly Ser Glu Pro Arg Ala His Pro Ser Arg Arg Thr Ser Ile Leu Met	
60 65 70	
aga tca tca acg ccg cca aga agg tga aag ccg acg cgg tct acc cgg	591
Arg Ser Ser Thr Pro Pro Arg Arg Lys Arg Thr Arg Ser Thr Arg	
75 80 85	
ggt atg gtt tcc ttt cgg aaa atg ccc agc tcg cgc gtg aat gcg cgg	639
Gly Met Val Ser Phe Arg Lys Met Pro Ser Ser Arg Val Asn Ala Arg	
90 95 100 105	
aga acg gca tta cct tca tcg gtc cca ccc cgg agg tgc tcg acc tca	687
Arg Thr Ala Leu Pro Ser Ser Val Pro Pro Arg Arg Cys Ser Thr Ser	
110 115 120	
cgg gcg aca agt cca agg ctg tgt ccg ccg cga aga agg ccg ggc tgc	735
Arg Ala Thr Ser Pro Arg Leu Cys Pro Pro Arg Arg Arg Pro Gly Cys	
125 130 135	
cgg tgc tgg cgg aat cca ccc cca gca ccg aca tcg atg aga tcg tca	783
Arg Cys Trp Arg Asn Pro Pro Pro Ala Pro Thr Ser Met Arg Ser Ser	
140 145 150	
aga gtg ccg agg ggc aga cct acc cga tct tcg tca agg ccg tcg cag	831
Arg Val Pro Arg Gly Arg Pro Thr Arg Ser Ser Ser Arg Pro Ser Gln	
155 160 165	
gtg gtg gcg ggc gtg gta tgc ggt tcg tcg aga agc ccg agg acc tgc	879
Val Val Ala Gly Val Val Cys Gly Ser Ser Arg Ser Pro Arg Thr Cys	
170 175 180 185	
gtg agc tgg cca ggg agg cct ccc gcg agg cgg agg ccg ctt tcg gtg	927
Val Ser Trp Pro Gly Arg Pro Pro Ala Arg Arg Arg Pro Leu Ser Val	
190 195 200	

acg gat ccg tct acg tcg aac ggg ccg tga tca aac ccc agc aca tcg	975
Thr Asp Pro Ser Thr Ser Asn Gly Pro Ser Asn Pro Ser Thr Ser	
205 210 215	
agg tgc aga tcc tcg gtg atc aca ccg gcg atg tca tcc acc tgt atg	1023
Arg Cys Arg Ser Ser Val Ile Thr Pro Ala Met Ser Ser Thr Cys Met	
220 225 230	
aac gcg act gtt ccc tgc agc gcc gcc acc aga agg tcg tgg aga tcg	1071
Asn Ala Thr Val Pro Cys Ser Ala Ala Thr Arg Arg Ser Trp Arg Ser	
235 240 245	
cac ctg ccc agc acc tcg acc cgg agc tgc gcg acc gca tct gtg ccg	1119
His Leu Pro Ser Thr Ser Thr Arg Ser Cys Ala Thr Ala Ser Val Pro	
250 255 260	
atg ccg tga agt tct gca aat cca tcg gat acc agg gcg ccg gca ccg	1167
Met Pro Ser Ser Ala Asn Pro Ser Asp Thr Arg Ala Pro Ala Pro	
265 270 275	
tgg agt tcc tcg tcg acg agg cgg gca acc acg tct tca ttg aga tga	1215
Trp Ser Ser Ser Ser Thr Arg Arg Ala Thr Thr Ser Ser Leu Arg	
280 285 290	
acc ccc gca tcc agg tgg aac aca ccg tga ccg agg agg tca cct ccg	1263
Thr Pro Ala Ser Arg Trp Asn Thr Pro Pro Arg Arg Ser Pro Pro	
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Ser Thr Trp Ser Arg Arg Arg Cys Thr Trp Pro Pro Val Pro Pro	
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Arg Asn Trp Ala Pro Arg Thr Arg Ser Pro Pro Thr Val Pro Pro	
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Cys Ser Ala Ala Ser Pro Arg Arg Thr Arg Pro Thr Thr Ser Gly Pro	
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Thr Pro Val Ser Pro Pro Thr Ala Pro Arg Val Val Arg Val Cys	
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Val Ser Thr Ala Gln Pro Ser Ser Ala Ala Arg Ser Pro His Ile Ser	
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Ile Pro Cys Trp Ser Arg Pro Ala Ala Val Pro Ile Ser Arg Pro	
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Pro Cys Pro Glu Pro Ser Ala Pro Trp Arg Ser Ser Thr Ser Pro Ala	
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Trp Pro Pro Thr Ser Ala Ser Cys Val Arg Cys Cys Ala Arg Lys Thr	
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Ser	Pro	Arg	Gly	Ala	Ser	Thr	Pro	Ala	Ser	Ser	Ala	Pro	Thr	Ser	Thr		
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Cys	Ser	Arg	Pro	His	Arg	Pro	Thr	Met	Ser	Arg	Gly	Gly	Ser	Trp	Asn		
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Thr	Trp	Arg	Met	Ser	Pro		Thr	Asn	Pro	Thr	Val	Asn	Ala	Pro	Arg		
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Gln	Pro	Val	Arg		Arg	Ser	Cys	Pro	Arg	Trp	Arg	Thr	Ser	Arg	Cys		
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cac	gcg	gct	ccc	gcg	acc	gcc	tga	agc	agc	tgc	gcc	cgg	agg	gtt	tgc	1887	
His	Ala	Ala	Pro	Ala	Thr	Ala		Ser	Ser	Ser	Ala	Arg	Arg	Val	Ser		
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Pro	Ala	Ile	Cys	Ala	Asn	Arg	Met	Pro	Trp	Pro	Ser	Pro	Thr	Pro	Pro		
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tcc	gcg	atg	ccc	acc	agt	ccc	tcc	tgg	cca	ccc	gcg	tgc	gct	cct	tgc	1983	
Ser	Ala	Met	Pro	Thr	Ser	Pro	Ser	Trp	Pro	Pro	Ala	Cys	Ala	Pro	Ser		
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cgc	tga	ccc	cgg	cgg	cgc	gcg	ccg	tgc	caa	agc	tca	ccc	ccg	agc	tgc	2031	
Arg		Pro	Arg	Arg	Arg	Ala	Pro	Ser	Gln	Ser	Ser	Pro	Pro	Ser	Cys		
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Cys	Arg	Trp	Arg	Pro	Gly	Ala	Val	Pro	Pro	Thr	Thr	Trp	Pro	Cys	Ala		
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Ser	Ser	Ser	Arg	Ile	Arg	Gly	His	Ala	Trp	Met	Ser	Cys	Val	Arg	Arg		
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Cys	Arg	Met		Thr	Ser	Arg	Cys	Cys	Cys	Val	Val	Ala	Thr	Pro	Ser		
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Gly	Thr	Pro	Arg	Thr	Pro	Ile	Arg	Cys	Ala	Ala	Arg	Leu	Cys	Arg	Arg		
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Pro	Pro	Ser	Pro	Val	Trp	Thr	Ser	Ser	Ala	Ser	Ser	Thr	Arg	Ser	Thr		
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Thr	Ser	Pro	Arg	Cys	Ala	Arg	Pro	Ser	Thr	Pro	Ser	Trp	Arg	Pro	Ala		
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cca	gtg	ttg	ccg	agg	tgc	cca	tgg	cgt	act	ccg	gtg	acc	tgt	cca	atc	2367	
Pro	Val	Leu	Pro	Arg	Ser	Pro	Trp	Arg	Thr	Pro	Val	Thr	Cys	Pro	Ile		
		655					660					665					
cgg	ggg	aga	agc	tct	aca	ccc	tgg	act	act	acc	tga	acc	tgg	ccg	agc	2415	
Arg	Gly	Arg	Ser	Ser	Thr	Pro	Trp	Thr	Thr	Thr		Thr	Trp	Pro	Ser		

670	675	680	
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gcc tgc tgc gcc gcg ccg cgg cgc cca aac tgg tca ccg ccc tgc gcc Ala Cys Cys Ala Ala Pro Arg Arg Pro Asn Trp Ser Pro Pro Cys Ala 700 705 710 715			2511
gtg aat tcg acc tgc ccg tgc atg tcc aca ccc acg aca ccg ccg gcg Val Asn Ser Thr Cys Pro Cys Met Ser Thr Pro Thr Thr Pro Pro Ala 720 725 730			2559
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ccg gtg gct ggc ccg aac cgc tgc gca ccc gtg cac tcg agg gtc gct Pro Val Ala Gly Pro Asn Arg Cys Ala Pro Val His Ser Arg Val Ala 910 915 920			3135

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4012

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<212> PRT
<213> Corynebacterium thermoaminogenes

<400> 24

Trp Leu Gln Gln His Pro Pro Arg Cys Arg Arg Ser Lys Arg Ser Trp
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Trp Pro Thr Glu Val Lys Ser Arg Cys Glu His Ser Ala Pro Pro Thr
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Arg Pro Gly Pro Gln Pro Trp Pro Ser Thr Pro Gly Arg Thr Val Ala
35 40 45

Pro Ser Thr Ala Pro Ser Pro Pro Arg Arg
50 55

<210> 25
<211> 24
<212> PRT
<213> Corynebacterium thermoaminogenes

<400> 25

Gly Ser Glu Pro Arg Ala His Pro Ser Arg Arg Thr Ser Ile Leu Met
1 5 10 15

Arg Ser Ser Thr Pro Pro Arg Arg
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<210> 26
<211> 128
<212> PRT
<213> Corynebacterium thermoaminogenes

<400> 26

Lys Arg Thr Arg Ser Thr Arg Gly Met Val Ser Phe Arg Lys Met Pro
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Ser Ser Arg Val Asn Ala Arg Arg Thr Ala Leu Pro Ser Ser Val Pro
20 25 30

Pro Arg Arg Cys Ser Thr Ser Arg Ala Thr Ser Pro Arg Leu Cys Pro
35 40 45

Pro Arg Arg Arg Pro Gly Cys Arg Cys Trp Arg Asn Pro Pro Pro Ala

50

55

60

Pro Thr Ser Met Arg Ser Ser Arg Val Pro Arg Gly Arg Pro Thr Arg
65 70 75 80

Ser Ser Ser Arg Pro Ser Gln Val Val Ala Gly Val Val Cys Gly Ser
85 90 95

Ser Arg Ser Pro Arg Thr Cys Val Ser Trp Pro Gly Arg Pro Pro Ala
100 105 110

Arg Arg Arg Pro Leu Ser Val Thr Asp Pro Ser Thr Ser Asn Gly Pro
115 120 125

<210> 27

<211> 56

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 27

Ser Asn Pro Ser Thr Ser Arg Cys Arg Ser Ser Val Ile Thr Pro Ala
1 5 10 15

Met Ser Ser Thr Cys Met Asn Ala Thr Val Pro Cys Ser Ala Ala Thr
20 25 30

Arg Arg Ser Trp Arg Ser His Leu Pro Ser Thr Ser Thr Arg Ser Cys
35 40 45

Ala Thr Ala Ser Val Pro Met Pro
50 55

<210> 28

<211> 28

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 28

Ser Ser Ala Asn Pro Ser Asp Thr Arg Ala Pro Ala Pro Trp Ser Ser
1 5 10 15

Ser Ser Thr Arg Arg Ala Thr Thr Ser Ser Leu Arg
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<210> 29

<211> 9

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<213> Corynebacterium thermoaminogenes

<400> 29

Thr Pro Ala Ser Arg Trp Asn Thr Pro
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<210> 30

<211> 21

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 30

Pro Arg Arg Ser Pro Pro Ser Thr Trp Ser Arg Arg Arg Cys Thr Trp
1 5 10 15

Pro Pro Val Pro Pro
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<210> 31

<211> 4

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 31

Arg Asn Trp Ala
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<210> 32

<211> 30

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 32

Pro Arg Thr Arg Ser Pro Pro Thr Val Pro Pro Cys Ser Ala Ala Ser
1 5 10 15

Pro Arg Arg Thr Arg Pro Thr Thr Ser Gly Pro Thr Pro Val
20 25 30

<210> 33

<211> 34

<212> PRT

<213> Corynebacterium thermoaminogenes

<400> 33

Ser Pro Pro Thr Ala Pro Arg Val Val Arg Val Cys Val Ser Thr Ala
1 5 10 15

Gln Pro Ser Ser Ala Ala Arg Ser Pro His Ile Ser Ile Pro Cys Trp
20 25 30

Ser Arg

<210> 34
<211> 79
<212> PRT
<213> Corynebacterium thermoaminogenes

<400> 34

Pro Ala Ala Val Pro Ile Ser Arg Pro Pro Cys Pro Glu Pro Ser Ala
1 5 10 15

Pro Trp Arg Ser Ser Thr Ser Pro Ala Trp Pro Pro Thr Ser Ala Ser
20 25 30

Cys Val Arg Cys Cys Ala Arg Lys Thr Ser Pro Arg Gly Ala Ser Thr
35 40 45

Pro Ala Ser Ser Ala Pro Thr Ser Thr Cys Ser Arg Pro His Arg Pro
50 55 60

Thr Met Ser Arg Gly Gly Ser Trp Asn Thr Trp Arg Met Ser Pro
65 70 75

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<400> 35

Thr Asn Pro Thr Val Asn Ala Pro Arg Gln Pro Val Arg
1 5 10

<210> 36
<211> 18
<212> PRT
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<400> 36

Arg Ser Cys Pro Arg Trp Arg Thr Ser Arg Cys His Ala Ala Pro Ala
1 5 10 15

Thr Ala

<210> 37
<211> 41

<212> PRT
<213> Corynebacterium thermoaminogenes

<400> 37

Ser Ser Ser Ala Arg Arg Val Ser Pro Ala Ile Cys Ala Asn Arg Met
1 5 10 15

Pro Trp Pro Ser Pro Thr Pro Pro Ser Ala Met Pro Thr Ser Pro Ser
20 25 30

Trp Pro Pro Ala Cys Ala Pro Ser Arg
35 40

<210> 38
<211> 49
<212> PRT
<213> Corynebacterium thermoaminogenes

<400> 38

Pro Arg Arg Arg Ala Pro Ser Gln Ser Ser Pro Pro Ser Cys Cys Arg
1 5 10 15

Trp Arg Pro Gly Ala Val Pro Pro Thr Thr Trp Pro Cys Ala Ser Ser
20 25 30

Ser Arg Ile Arg Gly His Ala Trp Met Ser Cys Val Arg Arg Cys Arg
35 40 45

Met

<210> 39
<211> 87
<212> PRT
<213> Corynebacterium thermoaminogenes

<400> 39

Thr Ser Arg Cys Cys Cys Val Val Ala Thr Pro Ser Gly Thr Pro Arg
1 5 10 15

Thr Pro Ile Arg Cys Ala Ala Arg Leu Cys Arg Arg Pro Pro Ser Pro
20 25 30

Val Trp Thr Ser Ser Ala Ser Ser Thr Arg Ser Thr Thr Ser Pro Arg
35 40 45

Cys Ala Arg Pro Ser Thr Pro Ser Trp Arg Pro Ala Pro Val Leu Pro
50 55 60

Arg Ser Pro Trp Arg Thr Pro Val Thr Cys Pro Ile Arg Gly Arg Ser
65 70 75 80

Ser Thr Pro Trp Thr Thr Thr
85

<210> 40
<211> 198
<212> PRT
<213> Corynebacterium thermoaminogenes

<400> 40

Thr Trp Pro Ser Arg Ser Ser Thr Pro Val His Thr Ser Trp Pro Ser
1 5 10 15

Arg Thr Trp Pro Ala Cys Cys Ala Ala Pro Arg Arg Pro Asn Trp Ser
20 25 30

Pro Pro Cys Ala Val Asn Ser Thr Cys Pro Cys Met Ser Thr Pro Thr
35 40 45

Thr Pro Pro Ala Val Ser Trp Pro Pro Thr Trp Pro Pro Pro Thr Pro
50 55 60

Gly Pro Met Pro Ser Thr Pro Pro Pro His Pro Cys Pro Val Pro Pro
65 70 75 80

Pro Ser Arg Arg Cys Pro Leu Trp Leu Pro Arg Leu Arg Thr Pro Asp
85 90 95

Ala Thr Pro Ala Ser Thr Cys Arg Pro Ser Pro Thr Trp Asn Arg Thr
100 105 110

Gly Arg Arg Ser Ala Asp Cys Thr Cys Arg Leu Asn Pro Ala Pro Arg
115 120 125

Ala Arg Pro Asp Ala Phe Thr Ala Thr Arg Ser Pro Ala Val Ser Cys
130 135 140

Pro Thr Cys Val Pro Arg Pro Leu His Trp Val Trp Pro Thr Ala Ser
145 150 155 160

Ser Ser Ser Arg Thr Thr Thr Arg Pro Ser Thr Arg Cys Trp Val Val
165 170 175

Arg Pro Arg Ser Pro Arg Pro Pro Arg Leu Ser Val Thr Ser His Cys
 180 185 190

Thr Ser Ser Val Pro Val
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<210> 41
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 <213> Corynebacterium thermoaminogenes
 <400> 41

Ala Arg Arg Ile Ser Pro Pro Ile Arg Arg Ser Thr Thr Ser Pro Ile
 1 5 10 15

Arg Ser Ser Pro Ser Ser Ala Ala Asn Trp Val Pro Leu Pro Val Ala
 20 25 30

Gly Pro Asn Arg Cys Ala Pro Val His Ser Arg Val Ala Pro Arg Val
 35 40 45

Arg Pro Arg Trp Arg Arg Ser Pro Pro Arg Ser Arg Pro Thr Trp Ile
 50 55 60

Pro Met Ile Pro Arg Ser Val Ala Ala Pro Ser Thr Ala Cys Cys Ser
 65 70 75 80

Arg Ser Arg Pro Arg Ser Ser Leu Ser Thr Val Ala Ala Ser Ala Thr
 85 90 95

Pro Pro Pro Trp Met Thr Ala Ser Ser Ser Thr Ala
 100 105

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 <400> 42

Arg Arg Asp Val Arg Ser
 1 5

<210> 43
 <211> 70
 <212> PRT
 <213> Corynebacterium thermoaminogenes
 <400> 43

Pro Val Cys Pro Pro Arg Trp Trp Ser Ala Trp Met Arg Cys Pro Asn
 1 5 10 15

Arg Met Thr Lys Ala Cys Ala Thr Trp Trp Ser Thr Ser Thr Ala Arg
 20 25 30

Ser Ala Arg Ser Arg Cys Ala Thr Val Pro Trp Ser Pro Ser Pro Pro
 35 40 45

Pro Arg Arg Arg Pro Met Pro Pro Thr Arg Ala Met Ser Pro His His
 50 55 60

Ser Pro Val Trp Ser Pro
 65 70

<210> 44
 <211> 19
 <212> PRT
 <213> Corynebacterium thermoaminogenes

<400> 44

Pro Ser Pro Arg Val Met Arg Ser Arg Leu Ala Thr Pro Trp Pro Ser
 1 5 10 15

Leu Arg Pro

<210> 45
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 <212> PRT
 <213> Corynebacterium thermoaminogenes

<400> 45

Arg Trp Arg Pro Pro Ser Pro Arg Leu Ser Thr Val Ser Ser Thr Ala
 1 5 10 15

Ser Trp Cys Pro Pro Pro Pro Arg Ser Arg Ala Ala Thr Ser Ser Trp
 20 25 30

Ser Cys Pro
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<210> 46
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<400> 46

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  Val Asn Glu Leu Leu Arg Asp Asp Ile Arg Tyr Leu Gly Arg Ile
    1              5              10              15

ctg ggc gag gtg atc tcc gag cag gag ggc cac cat gtc ttc gaa ctg      156
Leu Gly Glu Val Ile Ser Glu Gln Glu Gly His His Val Phe Glu Leu
              20              25              30

gtt gaa cgc gcc cgc cgg acc tcc ttc gac atc gcc aag gga cgc gcg      204
Val Glu Arg Ala Arg Arg Thr Ser Phe Asp Ile Ala Lys Gly Arg Ala
              35              40              45

gag atg gac agt ctg gtg gag gtg ttc gct ggc atc gac ccg gag gac      252
Glu Met Asp Ser Leu Val Glu Val Phe Ala Gly Ile Asp Pro Glu Asp
              50              55              60

gcc acg ccc gtg gcc cga gcc ttc acc cat ttc gcc ctg ttg gcc aac      300
Ala Thr Pro Val Ala Arg Ala Phe Thr His Phe Ala Leu Leu Ala Asn
    65              70              75

ctc gcg gag gat ttg cat gac gca gcc cag cgg gaa cag gcc ctg aac      348
Leu Ala Glu Asp Leu His Asp Ala Ala Gln Arg Glu Gln Ala Leu Asn
    80              85              90              95

tcg ggt gag ccc gcg ccg gac agc acc ctc gag gcc acc tgg gtg aaa      396
Ser Gly Glu Pro Ala Pro Asp Ser Thr Leu Glu Ala Thr Trp Val Lys
              100              105              110

ctg gat gat gcc ggg gtg ggc agc ggt gag gtc gcc gcg gtg atc cgc      444
Leu Asp Asp Ala Gly Val Gly Ser Gly Glu Val Ala Ala Val Ile Arg
              115              120              125

aat gcg ctc gtc gcc ccg gtg ctc acc gcg cac ccg acg gaa acc cga      492
Asn Ala Leu Val Ala Pro Val Thr Ala His Pro Thr Glu Thr Arg
              130              135              140

cgt cgt acc gtg ttc gac gcg cag aag cac atc acc gcc ctg atg gag      540
Arg Arg Thr Val Phe Asp Ala Gln Lys His Ile Thr Ala Leu Met Glu
              145              150              155

gaa cgc cac ctc ctc ctg gcg ctg ccc acg cat gcc cgg acc cag tcc      588
Glu Arg His Leu Leu Leu Ala Leu Pro Thr His Ala Arg Thr Gln Ser
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aag ctg gat gac atc gag cgc aac atc cgg cga cgg atc acg atc ctg      636
Lys Leu Asp Asp Ile Glu Arg Asn Ile Arg Arg Arg Ile Thr Ile Leu
              180              185              190

tgg cag acg gcc ctc atc cgt gtg gcc cgt ccc cgc atc gag gat gag      684
Trp Gln Thr Ala Leu Ile Arg Val Ala Arg Pro Arg Ile Glu Asp Glu
              195              200              205

gtc gag gtt gga ctg cgc tac tac aag ctc agc ctg ttg gcc gag atc      732
Val Glu Val Gly Leu Arg Tyr Tyr Lys Leu Ser Leu Leu Ala Glu Ile
              210              215              220
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ggg gac cat gat ggc aac ccc ttc gtc acc gcg gag act gtc acc tac Gly Asp His Asp Gly Asn Pro Phe Val Thr Ala Glu Thr Val Thr Tyr 260 265 270	876
gcc acc cat cgg gcc gcg gag acc gtg ctc aag tac tac gtc aag caa Ala Thr His Arg Ala Ala Glu Thr Val Leu Lys Tyr Tyr Val Lys Gln 275 280 285	924
ctg cac gcc ctg gaa cac gaa ctc agt ctc tcc gac cgg atg aac gtc Leu His Ala Leu Glu His Glu Leu Ser Leu Ser Asp Arg Met Asn Val 290 295 300	972
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gat gac atc atc gcc gat gac cgt ctg gcc atg ctg cgc tcg gcc ctg Asp Asp Ile Ile Ala Asp Asp Arg Leu Ala Met Leu Arg Ser Ala Leu 385 390 395	1260
gac agc ttc ggg ttc aac ctc tac tcc ctg gat ctg cgc cag aat tcc Asp Ser Phe Gly Phe Asn Leu Tyr Ser Leu Asp Leu Arg Gln Asn Ser 400 405 410 415	1308
gac ggt ttc gag gat gtc ctc acc gaa ttg ttc gcc acc gcc cag acc Asp Gly Phe Glu Asp Val Leu Thr Glu Leu Phe Ala Thr Ala Gln Thr 420 425 430	1356
gag aag aac tac cgc ggg ttg acg gag gcg gag aag ctg gac ctg ctg Glu Lys Asn Tyr Arg Gly Leu Thr Glu Ala Glu Lys Leu Asp Leu Leu 435 440 445	1404
atc cgc gaa ctg agc aca ccc cgc ccg ctc atc ccg cac ggg gac ccg Ile Arg Glu Leu Ser Thr Pro Arg Pro Leu Ile Pro His Gly Asp Pro 450 455 460	1452

gac tac tcc gag gcc acc aac cgt gaa ctg ggg att ttt tcg aag gcc Asp Tyr Ser Glu Ala Thr Asn Arg Glu Leu Gly Ile Phe Ser Lys Ala 465 470 475	1500
gcg gag gcc gtg cgt aaa ttc ggt cct ctc atg gtg ccg cac tgc atc Ala Glu Ala Val Arg Lys Phe Gly Pro Leu Met Val Pro His Cys Ile 480 485 490 495	1548
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gac gcg gag tta cgc ctg gtc gaa cta tgc cgg ggc cgt aat gtc aag Asp Ala Glu Leu Arg Leu Val Glu Leu Cys Arg Gly Arg Asn Val Lys 595 600 605	1884
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ccc tcc tat gat gcg atc ctg gcc cag ccc aag ggc gcg gtc cgg ggt Pro Ser Tyr Asp Ala Ile Leu Ala Gln Pro Lys Gly Ala Val Arg Gly 625 630 635	1980
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ctg gag gca tcg ctt ctg gat gat gtg gaa ctg ccc aat cgg gaa cgc Leu Glu Ala Ser Leu Leu Asp Asp Val Glu Leu Pro Asn Arg Glu Arg 675 680 685	2124
gcg cac cag atc atg ggg gag atc tcg gag ttg agc ttc cgc agg tac Ala His Gln Ile Met Gly Glu Ile Ser Glu Leu Ser Phe Arg Arg Tyr 690 695 700	2172
tca tca ctg gtc cat gag gat ccc gga ttc atc cag tac ttc acc cag	2220

Ser	Ser	Leu	Val	His	Glu	Asp	Pro	Gly	Phe	Ile	Gln	Tyr	Phe	Thr	Gln		
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Ser	Thr	Pro	Leu	Gln	Glu	Ile	Gly	Ser	Leu	Asn	Ile	Gly	Ser	Arg	Pro		
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tcc	tca	cgt	aaa	cag	acc	aac	acg	gtg	gag	gat	ctg	cgt	gcc	atc	ccg		2316
Ser	Ser	Arg	Lys	Gln	Thr	Asn	Thr	Val	Glu	Asp	Leu	Arg	Ala	Ile	Pro		
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tgg	gtg	ctc	agc	tgg	tcc	cag	tcc	cgt	gtc	atg	ctg	ccg	ggc	tgg	ttc		2364
Trp	Val	Leu	Ser	Trp	Ser	Gln	Ser	Arg	Val	Met	Leu	Pro	Gly	Trp	Phe		
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ggg	gtg	ggg	acc	gca	ctg	cgt	gag	tgg	atc	ggg	gag	ggg	gag	ggg	gct		2412
Gly	Val	Gly	Thr	Ala	Leu	Arg	Glu	Trp	Ile	Gly	Glu	Gly	Glu	Gly	Ala		
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gcg	gag	cgc	atc	gcg	gag	ctg	cag	gaa	ctc	aac	cgg	tgc	tgg	ccg	ttc		2460
Ala	Glu	Arg	Ile	Ala	Glu	Leu	Gln	Glu	Leu	Asn	Arg	Cys	Trp	Pro	Phe		
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Phe	Thr	Ser	Val	Leu	Asp	Asn	Met	Ala	Gln	Val	Met	Ser	Lys	Ala	Glu		
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ctg	cgc	ctg	gcc	agg	ttg	tac	gcc	gat	ctc	atc	ccg	gat	cgc	gag	gtg		2556
Leu	Arg	Leu	Ala	Arg	Leu	Tyr	Ala	Asp	Leu	Ile	Pro	Asp	Arg	Glu	Val		
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gcg	gac	cgg	atc	tat	gag	acc	atc	ttc	ggg	gag	tat	ttc	ctg	acc	aag		2604
Ala	Asp	Arg	Ile	Tyr	Glu	Thr	Ile	Phe	Gly	Glu	Tyr	Phe	Leu	Thr	Lys		
				835				840					845				
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Glu	Met	Phe	Cys	Thr	Ile	Thr	Gly	Ser	Gln	Asp	Leu	Leu	Asp	Asp	Asn		
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ccg	gcg	ctg	gcg	cga	tcg	gtg	cgc	agt	cgg	ttc	ccg	tac	ctg	ctg	ccg		2700
Pro	Ala	Leu	Ala	Arg	Ser	Val	Arg	Ser	Arg	Phe	Pro	Tyr	Leu	Leu	Pro		
				865			870				875						
ctc	aat	gtc	atc	cag	gtg	gag	atg	atg	cgc	cgg	tac	cgg	tcc	ggg	gat		2748
Leu	Asn	Val	Ile	Gln	Val	Glu	Met	Met	Arg	Arg	Tyr	Arg	Ser	Gly	Asp		
880					885					890					895		
gag	ggc	acg	gct	gtc	cca	cgt	aat	atc	cgc	ctg	acc	atg	aat	gga	ttg		2796
Glu	Gly	Thr	Ala	Val	Pro	Arg	Asn	Ile	Arg	Leu	Thr	Met	Asn	Gly	Leu		
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tcc	acg	gcc	ctg	cgc	aac	tcg	ggg	tagggcgcca	gacgccccgg	gaacccgcac							2850
Ser	Thr	Ala	Leu	Arg	Asn	Ser	Gly										
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 35 40 45

Met Asp Ser Leu Val Glu Val Phe Ala Gly Ile Asp Pro Glu Asp Ala
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Thr Pro Val Ala Arg Ala Phe Thr His Phe Ala Leu Leu Ala Asn Leu
 65 70 75 80

Ala Glu Asp Leu His Asp Ala Ala Gln Arg Glu Gln Ala Leu Asn Ser
 85 90 95

Gly Glu Pro Ala Pro Asp Ser Thr Leu Glu Ala Thr Trp Val Lys Leu
 100 105 110

Asp Asp Ala Gly Val Gly Ser Gly Glu Val Ala Ala Val Ile Arg Asn
 115 120 125

Ala Leu Val Ala Pro Val Leu Thr Ala His Pro Thr Glu Thr Arg Arg
 130 135 140

Arg Thr Val Phe Asp Ala Gln Lys His Ile Thr Ala Leu Met Glu Glu
 145 150 155 160

Arg His Leu Leu Leu Ala Leu Pro Thr His Ala Arg Thr Gln Ser Lys
 165 170 175

Leu Asp Asp Ile Glu Arg Asn Ile Arg Arg Arg Ile Thr Ile Leu Trp
 180 185 190

Gln Thr Ala Leu Ile Arg Val Ala Arg Pro Arg Ile Glu Asp Glu Val
 195 200 205

Glu Val Gly Leu Arg Tyr Tyr Lys Leu Ser Leu Leu Ala Glu Ile Pro
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Arg Ile Asn His Asp Val Thr Val Glu Leu Ala Arg Arg Phe Gly Gly
 225 230 235 240

Asp Ile Pro Thr Thr Ala Met Val Arg Pro Gly Ser Trp Ile Gly Gly
 245 250 255

Asp His Asp Gly Asn Pro Phe Val Thr Ala Glu Thr Val Thr Tyr Ala
 260 265 270

Thr His Arg Ala Ala Glu Thr Val Leu Lys Tyr Tyr Val Lys Gln Leu
 275 280 285

His Ala Leu Glu His Glu Leu Ser Leu Ser Asp Arg Met Asn Val Ile
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Ser Asp Glu Leu Arg Val Leu Ala Asp Ala Gly Gln Asn Asp Met Pro
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Ser Arg Val Asp Glu Pro Tyr Arg Arg Ala Ile His Gly Met Arg Gly
 325 330 335

Arg Met Leu Ala Thr Thr Ala Ala Leu Ile Gly Glu Glu Ala Val Glu
 340 345 350

Gly Thr Trp Phe Lys Thr Phe Thr Pro Tyr Thr Asp Thr His Glu Phe
 355 360 365

Lys Arg Asp Leu Asp Ile Val Asp Gly Ser Leu Arg Met Ser Arg Asp
 370 375 380

Asp Ile Ile Ala Asp Asp Arg Leu Ala Met Leu Arg Ser Ala Leu Asp
 385 390 395 400

Ser Phe Gly Phe Asn Leu Tyr Ser Leu Asp Leu Arg Gln Asn Ser Asp
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Gly Phe Glu Asp Val Leu Thr Glu Leu Phe Ala Thr Ala Gln Thr Glu
 420 425 430

Lys Asn Tyr Arg Gly Leu Thr Glu Ala Glu Lys Leu Asp Leu Leu Ile
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Arg Glu Leu Ser Thr Pro Arg Pro Leu Ile Pro His Gly Asp Pro Asp
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Tyr Ser Glu Ala Thr Asn Arg Glu Leu Gly Ile Phe Ser Lys Ala Ala
 465 470 475 480

Glu Ala Val Arg Lys Phe Gly Pro Leu Met Val Pro His Cys Ile Ile
 485 490 495

Ser Met Ala Ser Ser Val Thr Asp Ile Leu Glu Pro Met Val Leu Leu
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Lys Glu Phe Gly Leu Ile Arg Ala Asn Gly Lys Asn Pro Thr Gly Ser
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Val Asp Val Ile Pro Leu Phe Glu Thr Ile Asp Asp Leu Gln Arg Gly
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Ala Gly Ile Leu Glu Glu Leu Trp Asp Ile Asp Leu Tyr Arg Asn Tyr
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Leu Glu Gln Arg Asp Asn Val Gln Glu Val Met Leu Gly Tyr Ser Asp
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Ser Asn Lys Asp Gly Gly Tyr Phe Ala Ala Asn Trp Ala Leu Tyr Asp
 580 585 590

Ala Glu Leu Arg Leu Val Glu Leu Cys Arg Gly Arg Asn Val Lys Leu
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Arg Leu Phe His Gly Arg Gly Gly Thr Val Gly Arg Gly Gly Gly Pro
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Ser Tyr Asp Ala Ile Leu Ala Gln Pro Lys Gly Ala Val Arg Gly Ala
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Val Arg Val Thr Glu Gln Gly Glu Ile Ile Ser Ala Lys Tyr Gly Asn
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Pro Asp Thr Ala Arg Arg Asn Leu Glu Ala Leu Val Ser Ala Thr Leu

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His	Gln	Ile	Met	Gly	Glu	Ile	Ser	Glu	Leu	Ser	Phe	Arg	Arg	Tyr	Ser	
690					695					700						
Ser	Leu	Val	His	Glu	Asp	Pro	Gly	Phe	Ile	Gln	Tyr	Phe	Thr	Gln	Ser	
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Thr	Pro	Leu	Gln	Glu	Ile	Gly	Ser	Leu	Asn	Ile	Gly	Ser	Arg	Pro	Ser	
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Ser	Arg	Lys	Gln	Thr	Asn	Thr	Val	Glu	Asp	Leu	Arg	Ala	Ile	Pro	Trp	
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Val	Leu	Ser	Trp	Ser	Gln	Ser	Arg	Val	Met	Leu	Pro	Gly	Trp	Phe	Gly	
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Thr	Ser	Val	Leu	Asp	Asn	Met	Ala	Gln	Val	Met	Ser	Lys	Ala	Glu	Leu	
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Arg	Leu	Ala	Arg	Leu	Tyr	Ala	Asp	Leu	Ile	Pro	Asp	Arg	Glu	Val	Ala	
820					825					830						
Asp	Arg	Ile	Tyr	Glu	Thr	Ile	Phe	Gly	Glu	Tyr	Phe	Leu	Thr	Lys	Glu	
835					840					845						
Met	Phe	Cys	Thr	Ile	Thr	Gly	Ser	Gln	Asp	Leu	Leu	Asp	Asp	Asn	Pro	
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Ala	Leu	Ala	Arg	Ser	Val	Arg	Ser	Arg	Phe	Pro	Tyr	Leu	Leu	Pro	Leu	
865					870					875					880	
Asn	Val	Ile	Gln	Val	Glu	Met	Met	Arg	Arg	Tyr	Arg	Ser	Gly	Asp	Glu	
885					890					895						
Gly	Thr	Ala	Val	Pro	Arg	Asn	Ile	Arg	Leu	Thr	Met	Asn	Gly	Leu	Ser	
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tatagaaatt caaggggggat atcaa atg gct tct aat ttt aaa gaa aca gcg 712
Met Ala Ser Asn Phe Lys Glu Thr Ala
1 5
aag aaa caa ttt gat tta aat ggc caa tca tac acg tac tat gat tta 760
Lys Lys Gln Phe Asp Leu Asn Gly Gln Ser Tyr Thr Tyr Tyr Asp Leu
10 15 20 25
aaa tca tta gaa gaa caa ggt tta act aaa att tca aag tta cct tat 808
Lys Ser Leu Glu Glu Gln Gly Leu Thr Lys Ile Ser Lys Leu Pro Tyr
30 35 40
tca atc cgt gta tta cta gaa tca gtg tta cgt cag gaa gat gat ttt 856
Ser Ile Arg Val Leu Leu Glu Ser Val Leu Arg Gln Glu Asp Asp Phe
45 50 55
gta att act gat gat cac att aaa caa tta gca gaa ttt ggc aaa aaa 904
Val Ile Thr Asp Asp His Ile Lys Gln Leu Ala Glu Phe Gly Lys Lys
60 65 70
ggg aac gaa ggt gaa gta cct ttc aaa cca tct cga gtt att tta caa 952
Gly Asn Glu Gly Glu Val Pro Phe Lys Pro Ser Arg Val Ile Leu Gln

75	80	85	
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gca atg aat gat gtt ggt ggg gat att aat aaa att aac cct gaa gta Ala Met Asn Asp Val Gly Gly Asp Ile Asn Lys Ile Asn Pro Glu Val 110 115 120			1048
cca gtt gac tta gtt att gac cac tct gta caa gta gat agt tat gct Pro Val Asp Leu Val Ile Asp His Ser Val Gln Val Asp Ser Tyr Ala 125 130 135			1096
aat cca gat gca tta caa cgt aac atg aaa tta gaa ttt gaa cgt aac Asn Pro Asp Ala Leu Gln Arg Asn Met Lys Leu Glu Phe Glu Arg Asn 140 145 150			1144
tat gaa cgt tac caa ttc tta aac tgg gca aca aaa gca ttt gat aac Tyr Glu Arg Tyr Gln Phe Leu Asn Trp Ala Thr Lys Ala Phe Asp Asn 155 160 165			1192
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gaa tac tta gcg aat gtt gta cat gtt cgt gac gtt gac gga gaa caa Glu Tyr Leu Ala Asn Val Val His Val Arg Asp Val Asp Gly Glu Gln 190 195 200			1288
act gct ttc cca gat aca tta gtt ggt act gac tca cat act aca atg Thr Ala Phe Pro Asp Thr Leu Val Gly Thr Asp Ser His Thr Thr Met 205 210 215			1336
att aac ggt att ggt gta tta ggt tgg ggt gtc ggc ggt atc gaa gct Ile Asn Gly Ile Gly Val Leu Gly Trp Gly Val Gly Gly Ile Glu Ala 220 225 230			1384
gaa gca ggt atg tta gga caa cca tca tac ttc cca att cca gaa gtt Glu Ala Gly Met Leu Gly Gln Pro Ser Tyr Phe Pro Ile Pro Glu Val 235 240 245			1432
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Thr Gly Arg Lys Asp Asp His Ile Ala Leu Val Lys Glu Tyr Leu Gln	
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Gln Asn Asn Met Phe Phe Gln Val Glu Asn Glu Asp Pro Glu Tyr Thr	
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365 370 375	
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Pro Lys Arg Pro Gln Asp Leu Ile Phe Leu Ser Asp Met Lys Thr Glu	
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Phe Glu Lys Ser Val Thr Ala Pro Ala Gly Asn Gln Gly His Gly Leu	
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410 415 420 425	
aga act tca act atg aag act ggt gat gtt gcg att gca gcg att aca	2008
Arg Thr Ser Thr Met Lys Thr Gly Asp Val Ala Ile Ala Ala Ile Thr	
430 435 440	
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Ser Cys Thr Asn Thr Ser Asn Pro Tyr Val Met Leu Gly Ala Gly Leu	
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Val Ala Lys Lys Ala Ile Glu Lys Gly Leu Lys Val Pro Asp Tyr Val	
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Lys Thr Ser Leu Ala Pro Gly Ser Lys Val Val Thr Gly Tyr Leu Arg	
475 480 485	
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Gly Tyr Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu Leu Pro	
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Glu Ile Glu Lys Ala Val Ala Asp Glu Asp Leu Leu Val Thr Ser Val	
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Leu Ser Gly Asn Arg Asn Phe Glu Gly Arg Ile His Pro Leu Val Lys	
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gaa tat gca aat gta tac gaa aat aat gaa atg tgg aat gaa atc gac Glu Tyr Ala Asn Val Tyr Glu Asn Asn Glu Met Trp Asn Glu Ile Asp 620 625 630	2584
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gaa cca tta aaa gat tta cgt att atg ggt aaa ttt ggt gat tca gtt Glu Pro Leu Lys Asp Leu Arg Ile Met Gly Lys Phe Gly Asp Ser Val 670 675 680	2728
aca act gac cac att tct cca gca ggt gcg atc ggt aaa gat aca cca Thr Thr Asp His Ile Ser Pro Ala Gly Ala Ile Gly Lys Asp Thr Pro 685 690 695	2776
gca ggt aaa tat tta tta gac cat gat gtt cca att aga gaa ttt aac Ala Gly Lys Tyr Leu Leu Asp His Asp Val Pro Ile Arg Glu Phe Asn 700 705 710	2824
tct tat ggt tca aga cgt ggt aac cat gaa gta atg gta cgt ggt act Ser Tyr Gly Ser Arg Arg Gly Asn His Glu Val Met Val Arg Gly Thr 715 720 725	2872
ttc gct aat atc cgt att aaa aac caa tta gca cca ggc act gaa ggt Phe Ala Asn Ile Arg Ile Lys Asn Gln Leu Ala Pro Gly Thr Glu Gly 730 735 740 745	2920
gga ttt aca aca tat tgg cct aca gaa gaa atc atg cct atc tat gat Gly Phe Thr Thr Tyr Trp Pro Thr Glu Glu Ile Met Pro Ile Tyr Asp 750 755 760	2968
gca gct atg aga tac aaa gaa aat ggt act ggt tta gct gtt tta gct Ala Ala Met Arg Tyr Lys Glu Asn Gly Thr Gly Leu Ala Val Leu Ala 765 770 775	3016
ggt aat gat tac ggt atg ggt tca tct cgt gac tgg gca gct aaa ggt Gly Asn Asp Tyr Gly Met Gly Ser Ser Arg Asp Trp Ala Ala Lys Gly 780 785 790	3064
act aac tta tta ggt gtt aaa act gtt att gca caa agt tat gaa cgt Thr Asn Leu Leu Gly Val Lys Thr Val Ile Ala Gln Ser Tyr Glu Arg 795 800 805	3112
atc cat cgt tca aac tta gta atg atg ggt gta tta cca tta caa ttt	3160

Ile His Arg Ser Asn Leu Val Met Met Gly Val Leu Pro Leu Gln Phe
 810 815 820 825

aaa caa ggt gag tca gct gat tct cta ggt tta gaa ggt aaa gaa gaa 3208
 Lys Gln Gly Glu Ser Ala Asp Ser Leu Gly Leu Glu Gly Lys Glu Glu
 830 835 840

att tct gta gat atc gat gaa aat gtt aaa cca cat gat tta gta act 3256
 Ile Ser Val Asp Ile Asp Glu Asn Val Lys Pro His Asp Leu Val Thr
 845 850 855

gtt cat gct aaa aaa gaa aac gga gaa gtt gtt gat ttt gaa gca atg 3304
 Val His Ala Lys Lys Glu Asn Gly Glu Val Val Asp Phe Glu Ala Met
 860 865 870

gtt cgt ttc gat tca tta gta gaa tta gat tat tat cgt cat ggt ggt 3352
 Val Arg Phe Asp Ser Leu Val Glu Leu Asp Tyr Tyr Arg His Gly Gly
 875 880 885

atc tta caa atg gta tta aga aac aaa tta gct caa taatcacaat 3398
 Ile Leu Gln Met Val Leu Arg Asn Lys Leu Ala Gln
 890 895 900

gtgacttttg acagtgttaa cgtttaggtt agcactgttt ttttatgcta aactatatat 3458
 gtaatgttaa tagttaagga aggattggac ttaaattgatt tatagtttga ctgaaattga 3518
 accaagatat caagagacag ataaaatggg cgtgatttat catggcaatt atgcaacatg 3578
 gtttgaagta gcgcgtacag attacattag aaaactagga tttagttatg ctgatatgga 3638
 aaagcaaggg atcattttctc cagttacaga cttaaataatc aaatataaaa aatcaatttt 3698
 ttatcctgaa aaagtaacca ttaaaacatg ggtggaaaaa tattcaagat tacgttctgt 3758
 gtatagatat gaaatttttta atgaacaggg agaacttgca actacagggtt atactgagtt 3818
 aatttgatg aaagctgata ccttttagacc aattagatta gatcggttatt tctcagattg 3878
 gcatgaaacc tatagtaaag ttgaagctt 3907

<210> 49
 <211> 901
 <212> PRT
 <213> Corynebacterium thermoaminogenes

<400> 49

Met Ala Ser Asn Phe Lys Glu Thr Ala Lys Lys Gln Phe Asp Leu Asn
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Gly Gln Ser Tyr Thr Tyr Tyr Asp Leu Lys Ser Leu Glu Glu Gln Gly
 20 25 30

Leu Thr Lys Ile Ser Lys Leu Pro Tyr Ser Ile Arg Val Leu Leu Glu
 35 40 45

Ser Val Leu Arg Gln Glu Asp Asp Phe Val Ile Thr Asp Asp His Ile
 50 55 60

Lys Gln Leu Ala Glu Phe Gly Lys Lys Gly Asn Glu Gly Glu Val Pro
 65 70 75 80

Phe Lys Pro Ser Arg Val Ile Leu Gln Asp Phe Thr Gly Val Pro Ala
 85 90 95

Val Val Asp Leu Ala Ser Leu Arg Lys Ala Met Asn Asp Val Gly Gly
 100 105 110

Asp Ile Asn Lys Ile Asn Pro Glu Val Pro Val Asp Leu Val Ile Asp
 115 120 125

His Ser Val Gln Val Asp Ser Tyr Ala Asn Pro Asp Ala Leu Gln Arg
 130 135 140

Asn Met Lys Leu Glu Phe Glu Arg Asn Tyr Glu Arg Tyr Gln Phe Leu
 145 150 155 160

Asn Trp Ala Thr Lys Ala Phe Asp Asn Tyr Asn Ala Val Pro Pro Ala
 165 170 175

Thr Gly Ile Val His Gln Val Asn Leu Glu Tyr Leu Ala Asn Val Val
 180 185 190

His Val Arg Asp Val Asp Gly Glu Gln Thr Ala Phe Pro Asp Thr Leu
 195 200 205

Val Gly Thr Asp Ser His Thr Thr Met Ile Asn Gly Ile Gly Val Leu
 210 215 220

Gly Trp Gly Val Gly Gly Ile Glu Ala Glu Ala Gly Met Leu Gly Gln
 225 230 235 240

Pro Ser Tyr Phe Pro Ile Pro Glu Val Ile Gly Val Lys Leu Ser Asn
 245 250 255

Glu Leu Pro Gln Gly Ser Thr Ala Thr Asp Leu Ala Leu Arg Val Thr
 260 265 270

Glu Glu Leu Arg Lys Arg Gly Val Val Gly Lys Phe Val Glu Phe Phe
 275 280 285

Gly Pro Gly Val Thr Asn Leu Pro Leu Ala Asp Arg Ala Thr Ile Ala

290		295		300
Asn Met Ala Pro Glu Tyr Gly Ala Thr Cys Gly Phe Phe Pro Val Asp				
305		310	315	320
Glu Glu Ser Leu Lys Tyr Met Lys Leu Thr Gly Arg Lys Asp Asp His				
	325		330	335
Ile Ala Leu Val Lys Glu Tyr Leu Gln Gln Asn Asn Met Phe Phe Gln				
	340		345	350
Val Glu Asn Glu Asp Pro Glu Tyr Thr Glu Val Ile Asp Leu Asp Leu				
	355		360	365
Ser Thr Val Gln Ala Ser Leu Ser Gly Pro Lys Arg Pro Gln Asp Leu				
	370		375	380
Ile Phe Leu Ser Asp Met Lys Thr Glu Phe Glu Lys Ser Val Thr Ala				
385		390	395	400
Pro Ala Gly Asn Gln Gly His Gly Leu Asp Glu Ser Glu Phe Asp Lys				
	405		410	415
Lys Ala Glu Ile Lys Phe Asn Asp Gly Arg Thr Ser Thr Met Lys Thr				
	420		425	430
Gly Asp Val Ala Ile Ala Ala Ile Thr Ser Cys Thr Asn Thr Ser Asn				
	435		440	445
Pro Tyr Val Met Leu Gly Ala Gly Leu Val Ala Lys Lys Ala Ile Glu				
	450		455	460
Lys Gly Leu Lys Val Pro Asp Tyr Val Lys Thr Ser Leu Ala Pro Gly				
465		470	475	480
Ser Lys Val Val Thr Gly Tyr Leu Arg Asp Ser Gly Leu Gln Glu Tyr				
	485		490	495
Leu Asp Asp Leu Gly Phe Asn Leu Val Gly Tyr Gly Cys Thr Thr Cys				
	500		505	510
Ile Gly Asn Ser Gly Pro Leu Leu Pro Glu Ile Glu Lys Ala Val Ala				
	515		520	525
Asp Glu Asp Leu Leu Val Thr Ser Val Leu Ser Gly Asn Arg Asn Phe				
	530		535	540

Glu Gly Arg Ile His Pro Leu Val Lys Ala Asn Tyr Leu Ala Ser Pro
 545 550 555 560

Gln Leu Val Val Ala Tyr Ala Leu Ala Gly Thr Val Asp Ile Asp Leu
 565 570 575

His Asn Glu Pro Ile Gly Lys Gly Lys Asp Gly Glu Asp Val Tyr Leu
 580 585 590

Lys Asp Ile Trp Pro Ser Ile Lys Glu Val Ala Asp Thr Val Asp Ser
 595 600 605

Val Val Thr Pro Glu Leu Phe Leu Glu Glu Tyr Ala Asn Val Tyr Glu
 610 615 620

Asn Asn Glu Met Trp Asn Glu Ile Asp Val Thr Asp Ala Pro Leu Tyr
 625 630 635 640

Asp Phe Asp Pro Asn Ser Thr Tyr Ile Gln Asn Pro Ser Phe Phe Gln
 645 650 655

Gly Leu Ser Lys Glu Pro Gly Thr Ile Glu Pro Leu Lys Asp Leu Arg
 660 665 670

Ile Met Gly Lys Phe Gly Asp Ser Val Thr Thr Asp His Ile Ser Pro
 675 680 685

Ala Gly Ala Ile Gly Lys Asp Thr Pro Ala Gly Lys Tyr Leu Leu Asp
 690 695 700

His Asp Val Pro Ile Arg Glu Phe Asn Ser Tyr Gly Ser Arg Arg Gly
 705 710 715 720

Asn His Glu Val Met Val Arg Gly Thr Phe Ala Asn Ile Arg Ile Lys
 725 730 735

Asn Gln Leu Ala Pro Gly Thr Glu Gly Gly Phe Thr Thr Tyr Trp Pro
 740 745 750

Thr Glu Glu Ile Met Pro Ile Tyr Asp Ala Ala Met Arg Tyr Lys Glu
 755 760 765

Asn Gly Thr Gly Leu Ala Val Leu Ala Gly Asn Asp Tyr Gly Met Gly
 770 775 780

Ser Ser Arg Asp Trp Ala Ala Lys Gly Thr Asn Leu Leu Gly Val Lys
785 790 795 800

Thr Val Ile Ala Gln Ser Tyr Glu Arg Ile His Arg Ser Asn Leu Val
805 810 815

Met Met Gly Val Leu Pro Leu Gln Phe Lys Gln Gly Glu Ser Ala Asp
820 825 830

Ser Leu Gly Leu Glu Gly Lys Glu Glu Ile Ser Val Asp Ile Asp Glu
835 840 845

Asn Val Lys Pro His Asp Leu Val Thr Val His Ala Lys Lys Glu Asn
850 855 860

Gly Glu Val Val Asp Phe Glu Ala Met Val Arg Phe Asp Ser Leu Val
865 870 875 880

Glu Leu Asp Tyr Tyr Arg His Gly Gly Ile Leu Gln Met Val Leu Arg
885 890 895

Asn Lys Leu Ala Gln
900

<210> 50
<211> 3006
<212> DNA
<213> Corynebacterium thermoaminogenes

<220>
<221> CDS
<222> (328)..(2514)
<223>

<400> 50
gtcgcagcagc aacccccac cgccgaacca gccgccgatc tgggtgtggga gacacccggg 60
ttctcctccc tgggtgaaca ggtgccacaa ccccgctcca acaggcacac ctaccactgg 120
atcgccgggg agagcagcat ggtcacacgc ctgcggcgtg ccctggtgaa ggatcacggc 180
ctggacagat cgcaggtggc attcatgggt tattggaggc agggagtggc catgaggggt 240
tgatatcgct tccctgaggg tccgcaggcg tgcctcacc tgtattcttg atagttgaac 300
aaaagagccc acataacaag gagactc atg gct aag atc atc tgg acc cgc acc 354
Met Ala Lys Ile Ile Trp Thr Arg Thr
1 5
gac gaa gca ccg ctg ctc gcg acc tac tcg ctg aag ccg gtc gtc gag 402
Asp Glu Ala Pro Leu Leu Ala Thr Tyr Ser Leu Lys Pro Val Val Glu
10 15 20 25

gct ttc gcc gcc acc gcg ggc atc gag gtg gag acc cgc gat atc tct Ala Phe Ala Ala Thr Ala Gly Ile Glu Val Glu Thr Arg Asp Ile Ser 30 35 40	450
ctc gcc ggt cgc atc ctc gca cag ttc gcg gac cag ctc ccc gag gag Leu Ala Gly Arg Ile Leu Ala Gln Phe Ala Asp Gln Leu Pro Glu Glu 45 50 55	498
cag aag gtc tcc gac gcc ctc gcc gag ctc ggc gaa ctg gct aag acc Gln Lys Val Ser Asp Ala Leu Ala Glu Leu Gly Glu Leu Ala Lys Thr 60 65 70	546
ccc gaa gcc aac atc atc aag ctt ccc aac atc tcc gca tcc gta ccg Pro Glu Ala Asn Ile Ile Lys Leu Pro Asn Ile Ser Ala Ser Val Pro 75 80 85	594
cag ctc aag gct gcc gta aag gaa ctg cag gaa cag ggc tac gac ctg Gln Leu Lys Ala Ala Val Lys Glu Leu Gln Glu Gln Gly Tyr Asp Leu 90 95 100 105	642
ccc gag tac gag gat gcc aag gac cgc tac gcc gct gtc atc ggc tcc Pro Glu Tyr Glu Asp Ala Lys Asp Arg Tyr Ala Ala Val Ile Gly Ser 110 115 120	690
aac gtc aac ccg gtc ctg cgc gag ggc aac tcc gac cgc cgc gca ccg Asn Val Asn Pro Val Leu Arg Glu Gly Asn Ser Asp Arg Arg Ala Pro 125 130 135	738
gtg gcc gtg aag aac ttc gtg aag aag ttc ccc cac cgc atg ggc gag Val Ala Val Lys Asn Phe Val Lys Lys Phe Pro His Arg Met Gly Glu 140 145 150	786
tgg tcc gcc gac tcc aag acc aac gtt gcc acc atg ggt gcc gac gac Trp Ser Ala Asp Ser Lys Thr Asn Val Ala Thr Met Gly Ala Asp Asp 155 160 165	834
ttc cgc agc aat gag aag tcc gtg atc atg gac gag gcc gac acc gtg Phe Arg Ser Asn Glu Lys Ser Val Ile Met Asp Glu Ala Asp Thr Val 170 175 180 185	882
gtg atc aag cat gtc gcc gcc gac ggc acc gag acc gtg ctc aag gac Val Ile Lys His Val Ala Ala Asp Gly Thr Glu Thr Val Leu Lys Asp 190 195 200	930
agc ctc ccc ctg ctc aag ggt gag gtc atc gac ggc acc ttc atc tcc Ser Leu Pro Leu Leu Lys Gly Glu Val Ile Asp Gly Thr Phe Ile Ser 205 210 215	978
gcc aag gca ctg gac gcc ttc ctg ctc gac cag gtc aaa cgc gcc aag Ala Lys Ala Leu Asp Ala Phe Leu Leu Asp Gln Val Lys Arg Ala Lys 220 225 230	1026
gag gag ggc atc ctc ttc tcc gcc cac atg aag gcc acc atg atg aag Glu Glu Gly Ile Leu Phe Ser Ala His Met Lys Ala Thr Met Met Lys 235 240 245	1074
gtc tcc gac ccg atc atc ttc ggc cac atc gtc cgc gcc tac ttc gcc Val Ser Asp Pro Ile Ile Phe Gly His Ile Val Arg Ala Tyr Phe Ala 250 255 260 265	1122

gat gtc tac gca cag tac ggt gag cag ctg ctc gcc gcc ggc ctc aac	1170
Asp Val Tyr Ala Gln Tyr Gly Glu Gln Leu Leu Ala Ala Gly Leu Asn	
270 275 280	
ggg gag aac ggt ctc gcc gcc atc tac gcc ggc ctg gac aag ctg gac	1218
Gly Glu Asn Gly Leu Ala Ala Ile Tyr Ala Gly Leu Asp Lys Leu Asp	
285 290 295	
aac ggt gcc gag atc aag gca gcc ttc gac aag ggc ctg gaa gag ggc	1266
Asn Gly Ala Glu Ile Lys Ala Ala Phe Asp Lys Gly Leu Glu Glu Gly	
300 305 310	
ccc gac ctg gcc atg gtg aac tcc gcc aag ggc atc acc aac ctg cat	1314
Pro Asp Leu Ala Met Val Asn Ser Ala Lys Gly Ile Thr Asn Leu His	
315 320 325	
gtg ccc tcc gat gtc atc atc gac gcc tcc atg ccc gcc atg atc cgc	1362
Val Pro Ser Asp Val Ile Ile Asp Ala Ser Met Pro Ala Met Ile Arg	
330 335 340 345	
acc tcc ggc aag atg tgg aac aag gac gac cag acc cag gat gcc ctg	1410
Thr Ser Gly Lys Met Trp Asn Lys Asp Asp Gln Thr Gln Asp Ala Leu	
350 355 360	
gct gtc atc ccg gac tcc tcc tac gcc ggt gtc tac cag acc gtc atc	1458
Ala Val Ile Pro Asp Ser Ser Tyr Ala Gly Val Tyr Gln Thr Val Ile	
365 370 375	
gag gac tgc cgc aag aat ggc gcc ttc gat ccg acc acc atg ggc acc	1506
Glu Asp Cys Arg Lys Asn Gly Ala Phe Asp Pro Thr Thr Met Gly Thr	
380 385 390	
gtc ccc aac gtc ggt ctg atg gca cag aag gcc gag gag tac ggc tcc	1554
Val Pro Asn Val Gly Leu Met Ala Gln Lys Ala Glu Glu Tyr Gly Ser	
395 400 405	
cac gac aag acc ttc cgt atc gag gcc gac ggc aag gta cag gtc gtc	1602
His Asp Lys Thr Phe Arg Ile Glu Ala Asp Gly Lys Val Gln Val Val	
410 415 420 425	
gcc tcc aac ggt gat gtc ctc atc gag cac gac gtg gag aag ggc gac	1650
Ala Ser Asn Gly Asp Val Leu Ile Glu His Asp Val Glu Lys Gly Asp	
430 435 440	
atc tgg cgc gcc tgc cag acc aag gac gcc ccg atc cag gac tgg gtc	1698
Ile Trp Arg Ala Cys Gln Thr Lys Asp Ala Pro Ile Gln Asp Trp Val	
445 450 455	
aag ctg gct gtc aac cgc gca cgt ctc tcc ggc atg ccc gct gtg ttc	1746
Lys Leu Ala Val Asn Arg Ala Arg Leu Ser Gly Met Pro Ala Val Phe	
460 465 470	
tgg ctg gat ccc gcc cgc gca cac gac cgc aac ctg acc aca ctg gtg	1794
Trp Leu Asp Pro Ala Arg Ala His Asp Arg Asn Leu Thr Thr Leu Val	
475 480 485	
gag aag tac ctg gca gac cac gac acc gag ggc ctg gac atc cag atc	1842
Glu Lys Tyr Leu Ala Asp His Asp Thr Glu Gly Leu Asp Ile Gln Ile	
490 495 500 505	
ctc tcc ccc gtc gag gcc acc cag cac gcc atc gac cgc atc cgc cgc	1890

Leu	Ser	Pro	Val	Glu	Ala	Thr	Gln	His	Ala	Ile	Asp	Arg	Ile	Arg	Arg		
				510					515					520			
ggc	gag	gac	acc	atc	tcc	gtc	acc	ggg	aac	gtc	ctg	cgt	gac	tac	aac		1938
Gly	Glu	Asp	Thr	Ile	Ser	Val	Thr	Gly	Asn	Val	Leu	Arg	Asp	Tyr	Asn		
			525					530					535				
acc	gac	ctc	ttc	ccg	atc	ctc	gag	ctg	ggc	acc	tcc	gcc	aag	atg	ctc		1986
Thr	Asp	Leu	Phe	Pro	Ile	Leu	Glu	Leu	Gly	Thr	Ser	Ala	Lys	Met	Leu		
		540					545					550					
tcc	gtc	gtg	cca	ctg	atg	gcc	ggc	ggg	gga	ctc	ttc	gag	acc	ggg	gcc		2034
Ser	Val	Val	Pro	Leu	Met	Ala	Gly	Gly	Gly	Leu	Phe	Glu	Thr	Gly	Ala		
	555					560					565						
ggg	ggc	tcc	gcc	ccg	aag	cac	gtc	cag	cag	gtc	atc	gag	gaa	aac	cac		2082
Gly	Gly	Ser	Ala	Pro	Lys	His	Val	Gln	Gln	Val	Ile	Glu	Glu	Asn	His		
570					575					580					585		
ctg	cgc	tgg	gat	tcc	ctc	ggg	gag	ttc	ctg	gcc	ctg	gcc	gag	tcc	ttc		2130
Leu	Arg	Trp	Asp	Ser	Leu	Gly	Glu	Phe	Leu	Ala	Leu	Ala	Glu	Ser	Phe		
				590					595					600			
cgc	cac	gag	ctc	aac	acc	cgc	aac	aac	acc	aag	gcc	ggg	gtc	ctc	gcc		2178
Arg	His	Glu	Leu	Asn	Thr	Arg	Asn	Asn	Thr	Lys	Ala	Gly	Val	Leu	Ala		
			605					610					615				
gat	gcc	ctg	gac	cgt	gcg	acc	gag	aag	ctc	ctc	aac	gag	gag	aag	tcc		2226
Asp	Ala	Leu	Asp	Arg	Ala	Thr	Glu	Lys	Leu	Leu	Asn	Glu	Glu	Lys	Ser		
		620					625					630					
ccg	tcc	cgc	aag	gtc	ggc	gag	atc	gac	aac	cgt	ggg	tcc	cac	ttc	tgg		2274
Pro	Ser	Arg	Lys	Val	Gly	Glu	Ile	Asp	Asn	Arg	Gly	Ser	His	Phe	Trp		
	635					640					645						
ctg	gcc	acc	tac	tgg	gcc	gat	gaa	ctg	gcc	aac	cag	acc	gag	gac	gcc		2322
Leu	Ala	Thr	Tyr	Trp	Ala	Asp	Glu	Leu	Ala	Asn	Gln	Thr	Glu	Asp	Ala		
650					655				660						665		
gag	ctg	gct	gag	acc	ttc	gcc	cct	gtc	gcc	gag	gcc	ctg	aac	aac	cag		2370
Glu	Leu	Ala	Glu	Thr	Phe	Ala	Pro	Val	Ala	Glu	Ala	Leu	Asn	Asn	Gln		
			670					675					680				
gct	gcc	gac	atc	gac	gca	gca	ctc	atc	ggg	gag	cag	ggc	aag	cct	gtc		2418
Ala	Ala	Asp	Ile	Asp	Ala	Ala	Leu	Ile	Gly	Glu	Gln	Gly	Lys	Pro	Val		
		685						690					695				
gac	ctg	ggg	ggc	tac	tac	gca	ccc	tcc	gat	gag	aag	acc	tcc	gcg	atc		2466
Asp	Leu	Gly	Gly	Tyr	Tyr	Ala	Pro	Ser	Asp	Glu	Lys	Thr	Ser	Ala	Ile		
		700					705					710					
atg	cgc	ccg	gtg	gcc	gca	ttc	aac	gag	atc	atc	gac	tcc	ctg	aag	aag		2514
Met	Arg	Pro	Val	Ala	Ala	Phe	Asn	Glu	Ile	Ile	Asp	Ser	Leu	Lys	Lys		
	715					720					725						
taaccccttc	tcgggagccg	acagccgacg	gccacgctcc	cccgccacg	ggggatcggtg												2574
gccgtcggcc	gtttctggca	ctggagtga	cacttcggtg	ataatggtga	gatgaacagc												2634
ccccgtgtcc	ccgccatcct	gtccgcggtt	tcgcgctgg	gtctgatcgc	tgcgctgggc												2694

acccccgttg ccgtcgcaga caccatcacc gcggacaccg accgggaaac ctgcgtggcc 2754
 agccagaatg acaactccag cgtgatcagg ttctgggatg acctggaggc cgatgtccgt 2814
 gagcagcgcc tgaccgaact ggatgcacag gaccccggcc tcaagaacga catcgaggcc 2874
 ttcatcgccg aggacccggt agccccctcc gcagccgata tccagagacg gctggatgca 2934
 aatgacgccc gtgagggcct ggccatgctg ctacctgaat cccgcaccga ccccgaggtg 2994
 gtggacctgc ag 3006

<210> 51
 <211> 729
 <212> PRT
 <213> *Corynebacterium thermoaminogenes*

<400> 51

Met Ala Lys Ile Ile Trp Thr Arg Thr Asp Glu Ala Pro Leu Leu Ala
 1 5 10 15

Thr Tyr Ser Leu Lys Pro Val Val Glu Ala Phe Ala Ala Thr Ala Gly
 20 25 30

Ile Glu Val Glu Thr Arg Asp Ile Ser Leu Ala Gly Arg Ile Leu Ala
 35 40 45

Gln Phe Ala Asp Gln Leu Pro Glu Glu Gln Lys Val Ser Asp Ala Leu
 50 55 60

Ala Glu Leu Gly Glu Leu Ala Lys Thr Pro Glu Ala Asn Ile Ile Lys
 65 70 75 80

Leu Pro Asn Ile Ser Ala Ser Val Pro Gln Leu Lys Ala Ala Val Lys
 85 90 95

Glu Leu Gln Glu Gln Gly Tyr Asp Leu Pro Glu Tyr Glu Asp Ala Lys
 100 105 110

Asp Arg Tyr Ala Ala Val Ile Gly Ser Asn Val Asn Pro Val Leu Arg
 115 120 125

Glu Gly Asn Ser Asp Arg Arg Ala Pro Val Ala Val Lys Asn Phe Val
 130 135 140

Lys Lys Phe Pro His Arg Met Gly Glu Trp Ser Ala Asp Ser Lys Thr
 145 150 155 160

Asn Val Ala Thr Met Gly Ala Asp Asp Phe Arg Ser Asn Glu Lys Ser

165	170	175
Val Ile Met Asp Glu Ala Asp Thr Val Val Ile Lys His Val Ala Ala		
180	185	190
Asp Gly Thr Glu Thr Val Leu Lys Asp Ser Leu Pro Leu Leu Lys Gly		
195	200	205
Glu Val Ile Asp Gly Thr Phe Ile Ser Ala Lys Ala Leu Asp Ala Phe		
210	215	220
Leu Leu Asp Gln Val Lys Arg Ala Lys Glu Glu Gly Ile Leu Phe Ser		
225	230	235
Ala His Met Lys Ala Thr Met Met Lys Val Ser Asp Pro Ile Ile Phe		
245	250	255
Gly His Ile Val Arg Ala Tyr Phe Ala Asp Val Tyr Ala Gln Tyr Gly		
260	265	270
Glu Gln Leu Leu Ala Ala Gly Leu Asn Gly Glu Asn Gly Leu Ala Ala		
275	280	285
Ile Tyr Ala Gly Leu Asp Lys Leu Asp Asn Gly Ala Glu Ile Lys Ala		
290	295	300
Ala Phe Asp Lys Gly Leu Glu Glu Gly Pro Asp Leu Ala Met Val Asn		
305	310	315
Ser Ala Lys Gly Ile Thr Asn Leu His Val Pro Ser Asp Val Ile Ile		
325	330	335
Asp Ala Ser Met Pro Ala Met Ile Arg Thr Ser Gly Lys Met Trp Asn		
340	345	350
Lys Asp Asp Gln Thr Gln Asp Ala Leu Ala Val Ile Pro Asp Ser Ser		
355	360	365
Tyr Ala Gly Val Tyr Gln Thr Val Ile Glu Asp Cys Arg Lys Asn Gly		
370	375	380
Ala Phe Asp Pro Thr Thr Met Gly Thr Val Pro Asn Val Gly Leu Met		
385	390	395
Ala Gln Lys Ala Glu Glu Tyr Gly Ser His Asp Lys Thr Phe Arg Ile		
405	410	415

Glu Ala Asp Gly Lys Val Gln Val Val Ala Ser Asn Gly Asp Val Leu
 420 425 430

Ile Glu His Asp Val Glu Lys Gly Asp Ile Trp Arg Ala Cys Gln Thr
 435 440 445

Lys Asp Ala Pro Ile Gln Asp Trp Val Lys Leu Ala Val Asn Arg Ala
 450 455 460

Arg Leu Ser Gly Met Pro Ala Val Phe Trp Leu Asp Pro Ala Arg Ala
 465 470 475 480

His Asp Arg Asn Leu Thr Thr Leu Val Glu Lys Tyr Leu Ala Asp His
 485 490 495

Asp Thr Glu Gly Leu Asp Ile Gln Ile Leu Ser Pro Val Glu Ala Thr
 500 505 510

Gln His Ala Ile Asp Arg Ile Arg Arg Gly Glu Asp Thr Ile Ser Val
 515 520 525

Thr Gly Asn Val Leu Arg Asp Tyr Asn Thr Asp Leu Phe Pro Ile Leu
 530 535 540

Glu Leu Gly Thr Ser Ala Lys Met Leu Ser Val Val Pro Leu Met Ala
 545 550 555 560

Gly Gly Gly Leu Phe Glu Thr Gly Ala Gly Gly Ser Ala Pro Lys His
 565 570 575

Val Gln Gln Val Ile Glu Glu Asn His Leu Arg Trp Asp Ser Leu Gly
 580 585 590

Glu Phe Leu Ala Leu Ala Glu Ser Phe Arg His Glu Leu Asn Thr Arg
 595 600 605

Asn Asn Thr Lys Ala Gly Val Leu Ala Asp Ala Leu Asp Arg Ala Thr
 610 615 620

Glu Lys Leu Leu Asn Glu Glu Lys Ser Pro Ser Arg Lys Val Gly Glu
 625 630 635 640

Ile Asp Asn Arg Gly Ser His Phe Trp Leu Ala Thr Tyr Trp Ala Asp
 645 650 655

Glu Leu Ala Asn Gln Thr Glu Asp Ala Glu Leu Ala Glu Thr Phe Ala
660 665 670

Pro Val Ala Glu Ala Leu Asn Asn Gln Ala Ala Asp Ile Asp Ala Ala
675 680 685

Leu Ile Gly Glu Gln Gly Lys Pro Val Asp Leu Gly Gly Tyr Tyr Ala
690 695 700

Pro Ser Asp Glu Lys Thr Ser Ala Ile Met Arg Pro Val Ala Ala Phe
705 710 715 720

Asn Glu Ile Ile Asp Ser Leu Lys Lys
725

<210> 52
<211> 2322
<212> DNA
<213> Corynebacterium thermoaminogenes

<220>
<221> CDS
<222> (806)..(2212)
<223>

<400> 52
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tcataacgtc cttatgaatt tcgcagttat tagttattta aatagagaat caaactccga 120
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Val Thr Glu His Tyr Asp Val Val Val
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Cys Leu Asn Val Gly Cys Ile Pro Ser Lys Ala Leu Ile Lys Asn Ala	
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His Ala Thr Thr Ala Val Arg Asp Asn Gly Asp Ser Val Glu Val Asp	
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Lys Val Ser Ser Phe Pro Phe Ser Ala Asn Gly Lys Ala Val Gly Leu	
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Asn Glu Leu Val Leu Ala Gln Asn Trp Asp Leu Thr Thr Glu Glu Ile	
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Pro Ser Lys Ala Leu Ile Lys Asn Ala Glu Ile Ala His Ile Phe Asn
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His Glu Lys Lys Thr Phe Gly Ile Asn Gly Glu Val Thr Phe Asn Tyr
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Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile Thr Glu Ile Asp Gly
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Phe Gly Thr Phe Lys Asp Ala Lys Thr Ile Glu Val Thr Asp Gly Lys
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Asp Ala Gly Lys Thr Val Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly
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Ser Val Val Asn Ser Leu Arg Gly Val Glu Phe Ser Glu Asn Val Val
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Ser Tyr Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Lys Lys Met Val
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Ile Val Gly Gly Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Gly
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Asn Tyr Gly Val Asp Val Thr Leu Ile Glu Phe Met Asp Arg Val Leu
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Pro Asn Glu Asp Pro Glu Val Ser Lys Val Ile Ala Lys Ala Tyr Lys
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Lys Met Gly Ile Lys Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg
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Asp Asn Gly Asp Ser Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp
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Lys Thr Glu Thr Ile Thr Val Asp Arg Val Leu Ile Ser Val Gly Phe
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Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu Thr Asp Gly Phe Ala
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Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu Leu Gly Gly His Ile
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Val Gly Ala Asn Ala Ser Glu Leu Leu Asn Glu Leu Val Leu Ala Gln
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Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg Ser Val His Ile His
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Glu Trp Arg Glu Leu Phe Glu Ser Gln Gly Gly Pro Gln Ala Glu Lys
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gct acc ccc gcc acc ccc gaa gcc aag aag gca gct tcg tcg cag tcc      435
Ala Thr Pro Ala Thr Pro Glu Ala Lys Lys Ala Ala Ser Ser Gln Ser
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tca act tcc gga cag tcc acc gcc aag gct gcc cct gcc gcc aag acc      483
Ser Thr Ser Gly Gln Ser Thr Ala Lys Ala Ala Pro Ala Ala Lys Thr
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Ala Pro Ala Ser Ala Pro Ala Lys Ala Ala Pro Val Lys Gln Asn Gln
80              85              90

gcg tcc aag cct gcc aag aag gcc aag gag tcc ccc ctg tcc aag cca      579
Ala Ser Lys Pro Ala Lys Lys Ala Lys Glu Ser Pro Leu Ser Lys Pro
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Val	Asn	Asp	Gln	Leu	Lys	Arg	Thr	Arg	Gly	Gly	Lys	Ile	Ser	Phe	Thr	
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cac	atc	atc	ggc	tac	gcc	atg	gtg	aag	gct	gtc	atg	gca	cac	ccg	gac	819
His	Ile	Ile	Gly	Tyr	Ala	Met	Val	Lys	Ala	Val	Met	Ala	His	Pro	Asp	
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Pro	Glu	His	Ile	Asn	Leu	Gly	Leu	Ala	Ile	Asp	Leu	Pro	Gln	Lys	Asp	
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Leu	Thr	Asn	Pro	Gly	Gly	Ile	Gly	Thr	Arg	His	Ser	Ile	Pro	Arg	Leu	
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Thr	Lys	Gly	Gln	Gly	Thr	Ile	Ile	Gly	Val	Gly	Ser	Met	Asp	Tyr	Pro	
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Gly	Ala	Glu	Ser	Gly	Glu	Phe	Leu	Arg	Thr	Met	Ser	Gln	Leu	Leu	Val	
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Thr	Pro	Met	Arg	Trp	Ala	Gln	Asp	Leu	Pro	Asn	Thr	Gly	Val	Asp	Lys	
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Leu Gly Lys Met Lys Arg Pro Leu Val Val Phe Thr Pro Lys Ser	
1070 1075 1080	
atg ctg cgc aac aag gcc gcc acc tcc gct ccg gag gag ttc acc	3537
Met Leu Arg Asn Lys Ala Ala Thr Ser Ala Pro Glu Glu Phe Thr	
1085 1090 1095	
gag gtc acc cgc ttc aag tcc gtg atc gac gat ccg aac gtg gcg	3582
Glu Val Thr Arg Phe Lys Ser Val Ile Asp Asp Pro Asn Val Ala	
1100 1105 1110	
gat gcc tcc aag gtg aag aag atc atg ctg tgc tcc ggc aag atc	3627

Asp	Ala	Ser	Lys	Val	Lys	Lys	Ile	Met	Leu	Cys	Ser	Gly	Lys	Ile		
			1115					1120					1125			
tac	tac	gaa	ctg	gcc	aag	cgc	aag	gag	aag	gac	aac	cgc	gac	gac		3672
Tyr	Tyr	Glu	Leu	Ala	Lys	Arg	Lys	Glu	Lys	Asp	Asn	Arg	Asp	Asp		
			1130					1135					1140			
atc	gcg	atc	gtg	cgc	atc	gag	atg	ctg	cac	ccg	atc	ccg	ttc	aac		3717
Ile	Ala	Ile	Val	Arg	Ile	Glu	Met	Leu	His	Pro	Ile	Pro	Phe	Asn		
			1145					1150					1155			
cgt	ctg	cgc	gac	gcc	ttc	gac	ggc	tac	ccc	aac	gcc	gag	gag	atc		3762
Arg	Leu	Arg	Asp	Ala	Phe	Asp	Gly	Tyr	Pro	Asn	Ala	Glu	Glu	Ile		
			1160					1165					1170			
ctg	ttc	gtt	cag	gac	gag	ccg	gca	aac	cag	ggg	gcc	tgg	ccg	ttc		3807
Leu	Phe	Val	Gln	Asp	Glu	Pro	Ala	Asn	Gln	Gly	Ala	Trp	Pro	Phe		
			1175					1180					1185			
tac	cag	gag	cac	ctg	ccc	aac	ctc	atc	gag	ggc	atg	ctc	ccg	atg		3852
Tyr	Gln	Glu	His	Leu	Pro	Asn	Leu	Ile	Glu	Gly	Met	Leu	Pro	Met		
			1190					1195					1200			
cgt	cgc	atc	tgc	cgc	cgt	tcc	cag	tcc	tgc	act	gcg	acc	ggg	atc		3897
Arg	Arg	Ile	Ser	Arg	Arg	Ser	Gln	Ser	Ser	Thr	Ala	Thr	Gly	Ile		
			1205					1210					1215			
gcg	aag	gtg	cac	acc	atc	gag	cag	cag	aag	ctg	ctg	gat	gat	gcg		3942
Ala	Lys	Val	His	Thr	Ile	Glu	Gln	Gln	Lys	Leu	Leu	Asp	Asp	Ala		
			1220					1225					1230			
ttc	aac	gca	taa	acg	ttaa	tac	agc	ggt	gata	cct	tga	accc	cgcc	gcg		3991
Phe	Asn	Ala														

acccttttaga tgcggggcggg gttttgcttt gcctgcatag gcgataatat tcatatacac 4051

ccatcacggt taagttctgc atttggatcg tgcgagcatc ccggt 4096

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 <213> Corynebacterium thermoaminogenes

<400> 55

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Met	Phe	Gln	Gln	Phe	Lys	Lys	Asp	Pro	Gln	Ser	Val	Asp	Lys	Glu	Trp
			20					25					30		

Arg	Glu	Leu	Phe	Glu	Ser	Gln	Gly	Gly	Pro	Gln	Ala	Glu	Lys	Ala	Thr
		35					40					45			

Pro	Ala	Thr	Pro	Glu	Ala	Lys	Lys	Ala	Ala	Ser	Ser	Gln	Ser	Ser	Thr
	50					55				60					

Ser Gly Gln Ser Thr Ala Lys Ala Ala Pro Ala Ala Lys Thr Ala Pro
65 70 75 80

Ala Ser Ala Pro Ala Lys Ala Ala Pro Val Lys Gln Asn Gln Ala Ser
85 90 95

Lys Pro Ala Lys Lys Ala Lys Glu Ser Pro Leu Ser Lys Pro Ala Ala
100 105 110

Met Pro Glu Pro Gly Thr Thr Pro Leu Arg Gly Ile Phe Lys Ser Ile
115 120 125

Ala Lys Asn Met Asp Leu Ser Leu Glu Val Pro Thr Ala Thr Ser Val
130 135 140

Arg Asp Met Pro Ala Arg Leu Met Phe Glu Asn Arg Ala Met Val Asn
145 150 155 160

Asp Gln Leu Lys Arg Thr Arg Gly Gly Lys Ile Ser Phe Thr His Ile
165 170 175

Ile Gly Tyr Ala Met Val Lys Ala Val Met Ala His Pro Asp Met Asn
180 185 190

Asn Ser Tyr Asp Ile Val Asp Gly Lys Pro Ser Leu Val Val Pro Glu
195 200 205

His Ile Asn Leu Gly Leu Ala Ile Asp Leu Pro Gln Lys Asp Gly Ser
210 215 220

Arg Ala Leu Val Val Ala Ala Ile Lys Glu Thr Glu Lys Met Thr Phe
225 230 235 240

Ser Gln Phe Leu Glu Ala Tyr Glu Asp Val Val Ala Arg Ser Arg Val
245 250 255

Gly Lys Leu Thr Met Asp Asp Tyr Gln Gly Val Thr Ile Ser Leu Thr
260 265 270

Asn Pro Gly Gly Ile Gly Thr Arg His Ser Ile Pro Arg Leu Thr Lys
275 280 285

Gly Gln Gly Thr Ile Ile Gly Val Gly Ser Met Asp Tyr Pro Ala Glu
290 295 300

Phe Gln Gly Ala Ser Glu Asp Arg Leu Ala Glu Leu Gly Val Gly Lys
 305 310 315 320

Leu Val Thr Ile Thr Ser Thr Tyr Asp His Arg Val Ile Gln Gly Ala
 325 330 335

Glu Ser Gly Glu Phe Leu Arg Thr Met Ser Gln Leu Leu Val Asp Asp
 340 345 350

Ala Phe Trp Asp His Ile Phe Glu Glu Met Asn Val Pro Tyr Thr Pro
 355 360 365

Met Arg Trp Ala Gln Asp Leu Pro Asn Thr Gly Val Asp Lys Asn Thr
 370 375 380

Arg Val Met Gln Leu Ile Glu Ala Tyr Arg Ser Arg Gly His Leu Ile
 385 390 395 400

Ala Asp Thr Asn Pro Leu Pro Trp Val Gln Pro Gly Met Pro Val Pro
 405 410 415

Asp His Arg Asp Leu Asp Ile Glu Thr His Gly Leu Thr Leu Trp Asp
 420 425 430

Leu Asp Arg Thr Phe His Val Gly Gly Phe Gly Gly Lys Glu Thr Met
 435 440 445

Thr Leu Arg Glu Val Leu Ser Arg Leu Arg Ala Ala Tyr Thr Leu Lys
 450 455 460

Val Gly Ser Glu Tyr Thr His Ile Leu Asp Arg Asp Glu Arg Thr Trp
 465 470 475 480

Leu Gln Asp Arg Leu Glu Ala Gly Met Pro Lys Pro Thr Ala Ala Glu
 485 490 495

Gln Lys Tyr Ile Leu Gln Lys Leu Asn Ala Ala Glu Ala Phe Glu Asn
 500 505 510

Phe Leu Gln Thr Lys Tyr Val Gly Gln Lys Arg Phe Ser Leu Glu Gly
 515 520 525

Ala Glu Ser Leu Ile Pro Leu Met Asp Ser Ala Ile Asp Thr Ala Ala
 530 535 540

Gly Gln Gly Leu Asp Glu Val Val Ile Gly Met Pro His Arg Gly Arg
 545 550 555 560

Leu Asn Val Leu Phe Asn Ile Val Gly Lys Pro Leu Ala Ser Ile Phe
 565 570 575

Asn Glu Phe Glu Gly Gln Met Glu Gln Gly Gln Ile Gly Gly Ser Gly
 580 585 590

Asp Val Lys Tyr His Leu Gly Ser Glu Gly Thr His Leu Gln Met Phe
 595 600 605

Gly Asp Gly Glu Ile Lys Val Ser Leu Thr Ala Asn Pro Ser His Leu
 610 615 620

Glu Ala Val Asn Pro Val Val Glu Gly Ile Val Arg Ala Lys Gln Asp
 625 630 635 640

Ile Leu Asp Lys Gly Pro Asp Gly Tyr Thr Val Val Pro Leu Leu Leu
 645 650 655

His Gly Asp Ala Ala Phe Ala Gly Leu Gly Ile Val Pro Glu Thr Ile
 660 665 670

Asn Leu Ala Ala Leu Arg Gly Tyr Asp Val Gly Gly Thr Ile His Ile
 675 680 685

Val Val Asn Asn Gln Ile Gly Phe Thr Thr Thr Pro Asp Ser Ser Arg
 690 695 700

Ser Met His Tyr Ala Thr Asp Cys Ala Lys Ala Phe Gly Cys Pro Val
 705 710 715 720

Phe His Val Asn Gly Asp Asp Pro Glu Ala Val Val Trp Val Gly Gln
 725 730 735

Leu Ala Thr Glu Tyr Arg Arg Arg Phe Gly Lys Asp Val Phe Ile Asp
 740 745 750

Leu Ile Cys Tyr Arg Leu Arg Gly His Asn Glu Ala Asp Asp Pro Ser
 755 760 765

Met Thr Gln Pro Lys Met Tyr Glu Leu Ile Thr Gly Arg Asp Ser Val
 770 775 780

Arg Ala Thr Tyr Thr Glu Asp Leu Leu Gly Arg Gly Asp Leu Ser Pro

Leu Gln Leu Cys Ala Glu Gly Ser Met Thr Ile Ala Gln Pro Thr
 1040 1045 1050

Thr Pro Ala Asn Tyr Phe His Leu Leu Arg Arg His Ala Leu Gly
 1055 1060 1065

Lys Met Lys Arg Pro Leu Val Val Phe Thr Pro Lys Ser Met Leu
 1070 1075 1080

Arg Asn Lys Ala Ala Thr Ser Ala Pro Glu Glu Phe Thr Glu Val
 1085 1090 1095

Thr Arg Phe Lys Ser Val Ile Asp Asp Pro Asn Val Ala Asp Ala
 1100 1105 1110

Ser Lys Val Lys Lys Ile Met Leu Cys Ser Gly Lys Ile Tyr Tyr
 1115 1120 1125

Glu Leu Ala Lys Arg Lys Glu Lys Asp Asn Arg Asp Asp Ile Ala
 1130 1135 1140

Ile Val Arg Ile Glu Met Leu His Pro Ile Pro Phe Asn Arg Leu
 1145 1150 1155

Arg Asp Ala Phe Asp Gly Tyr Pro Asn Ala Glu Glu Ile Leu Phe
 1160 1165 1170

Val Gln Asp Glu Pro Ala Asn Gln Gly Ala Trp Pro Phe Tyr Gln
 1175 1180 1185

Glu His Leu Pro Asn Leu Ile Glu Gly Met Leu Pro Met Arg Arg
 1190 1195 1200

Ile Ser Arg Arg Ser Gln Ser Ser Thr Ala Thr Gly Ile Ala Lys
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Val His Thr Ile Glu Gln Gln Lys Leu Leu Asp Asp Ala Phe Asn
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<212> DNA

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<223> synthetic DNA

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<210> 59

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

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<400> 59

cggtgactgg gtgttccacc

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 agcagcgccc atgacggcga 20

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<400> 73

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<210> 74

<211> 20

<212> DNA

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<222> (9)..(9)
<223> n is inosine

<400> 76
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<210> 87
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<400> 87
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<210> 98
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<210> 99
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 <400> 99
 gcgcctgcag ccaccaggat gccctcaacc ag 32

<210> 100
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 <222> (1)..(1341)
 <223>

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 cgc aac gcc ggg gaa cct gag ttc cac cag gct gtc gcg gag gtt ctc 96
 Arg Asn Ala Gly Glu Pro Glu Phe His Gln Ala Val Ala Glu Val Leu
 20 25 30

 gaa tct ctg aag atc gtc ctg gag aag gac ccg cac tac gcc gac tac 144
 Glu Ser Leu Lys Ile Val Leu Glu Lys Asp Pro His Tyr Ala Asp Tyr
 35 40 45

 ggt ctg atc cag cgt ctc tgc gaa ccg gaa cgc cag ctg atc ttc cgt 192
 Gly Leu Ile Gln Arg Leu Cys Glu Pro Glu Arg Gln Leu Ile Phe Arg
 50 55 60

 gtg ccc tgg gtg gat gac aac ggt cag gtg cac gtc aac cgt ggt ttc 240
 Val Pro Trp Val Asp Asp Asn Gly Gln Val His Val Asn Arg Gly Phe
 65 70 75 80

 cgt gtc cag ttc aac tcc gca ctc ggc ccg tac aag ggt ggt ctg cgt 288
 Arg Val Gln Phe Asn Ser Ala Leu Gly Pro Tyr Lys Gly Gly Leu Arg
 85 90 95

 ttc cac ccc tcc gtc aac ctc ggc atc gtc aag ttc ctc ggc ttc gag 336
 Phe His Pro Ser Val Asn Leu Gly Ile Val Lys Phe Leu Gly Phe Glu

100	105	110	
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ggg ggt tcc gac ttc gac ccg aag ggc aag tcc gag ctg gag atc atg Gly Gly Ser Asp Phe Asp Pro Lys Gly Lys Ser Glu Leu Glu Ile Met 130 135 140			432
cgc ttc tgc cag tcc ttc atg acc gag ctg cac cgc cac atc ggc gag Arg Phe Cys Gln Ser Phe Met Thr Glu Leu His Arg His Ile Gly Glu 145 150 155 160			480
tac cgg gat gtc ccg gcc ggt gac atc gga gtc ggt ggc cgc gag atc Tyr Arg Asp Val Pro Ala Gly Asp Ile Gly Val Gly Gly Arg Glu Ile 165 170 175			528
ggg tac ctc ttc ggc cac tac cgc cgt ctg gcc aac cag cac gag tcc Gly Tyr Leu Phe Gly His Tyr Arg Arg Leu Ala Asn Gln His Glu Ser 180 185 190			576
ggg gtg ctc acc ggc aag ggc ctg acc tgg ggt ggt tcc ctg gtc cgc Gly Val Leu Thr Gly Lys Gly Leu Thr Trp Gly Gly Ser Leu Val Arg 195 200 205			624
acc gag gcc acc ggc ttc ggc acc gtc tac ttc gtc cag gag atg atc Thr Glu Ala Thr Gly Phe Gly Thr Val Tyr Phe Val Gln Glu Met Ile 210 215 220			672
aag gcg gaa ggg gag acc ctc gag ggc aag aag gtc atc gtc tcc ggt Lys Ala Glu Gly Glu Thr Leu Glu Gly Lys Lys Val Ile Val Ser Gly 225 230 235 240			720
tcc ggc aac gtg gcc acc tac gcc atc cag aag gtg cag gaa ctg ggt Ser Gly Asn Val Ala Thr Tyr Ala Ile Gln Lys Val Gln Glu Leu Gly 245 250 255			768
gcg gtt gtg gtc ggc ttc tcc gac tcc agc ggc tgg gtc tcc acc ccg Ala Val Val Val Gly Phe Ser Asp Ser Ser Gly Trp Val Ser Thr Pro 260 265 270			816
aac ggt gtt gac gtg gcc aag ctg cgt gag atc aag gag gtc cgt cgt Asn Gly Val Asp Val Ala Lys Leu Arg Glu Ile Lys Glu Val Arg Arg 275 280 285			864
gca cgc gtg tcc tcc tac gcc gac gag gtg gag ggt gcg gag tac cac Ala Arg Val Ser Ser Tyr Ala Asp Glu Val Glu Gly Ala Glu Tyr His 290 295 300			912
acc gac ggc tcc atc tgg gat ctg acc gcc gac atc gcg ctg ccc tgc Thr Asp Gly Ser Ile Trp Asp Leu Thr Ala Asp Ile Ala Leu Pro Cys 305 310 315 320			960
gcc acc cag aac gaa ctg gac ggc gac aac gcc cgc acc ctc gcg gac Ala Thr Gln Asn Glu Leu Asp Gly Asp Asn Ala Arg Thr Leu Ala Asp 325 330 335			1008
aac ggc tgc cgc ttc gtg gcg gag ggc gcc aac atg ccc tcc acc ccc Asn Gly Cys Arg Phe Val Ala Glu Gly Ala Asn Met Pro Ser Thr Pro 340 345 350			1056

gag gcc atc gac gtc ttc cgt gag cgt ggt gtt ctc ttc ggg ccg ggc	1104
Glu Ala Ile Asp Val Phe Arg Glu Arg Gly Val Leu Phe Gly Pro Gly	
355 360 365	
aag gct gcc aac gcc ggt ggc gtg gcc acc tcc gcc ctg gag atg cag	1152
Lys Ala Ala Asn Ala Gly Gly Val Ala Thr Ser Ala Leu Glu Met Gln	
370 375 380	
cag aac gcc tcc cgt gat tcc tgg agc ttc gag tac acc gat gag cgt	1200
Gln Asn Ala Ser Arg Asp Ser Trp Ser Phe Glu Tyr Thr Asp Glu Arg	
385 390 395 400	
ctc cac cgc atc atg aag aac atc ttc aag tcc tgc gcc gat acc gcc	1248
Leu His Arg Ile Met Lys Asn Ile Phe Lys Ser Cys Ala Asp Thr Ala	
405 410 415	
aag gag tac ggc cac gag aag aac tac gtg gtc ggt gcg aac atc gcc	1296
Lys Glu Tyr Gly His Glu Lys Asn Tyr Val Val Gly Ala Asn Ile Ala	
420 425 430	
gga ttc aag aag gtc gct gac gcc atg ctc gcc cag ggt gtc atc taa	1344
Gly Phe Lys Lys Val Ala Asp Ala Met Leu Ala Gln Gly Val Ile	
435 440 445	

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 <212> PRT
 <213> Corynebacterium thermoaminogenes

<400> 101

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Glu Ser Leu Lys Ile Val Leu Glu Lys Asp Pro His Tyr Ala Asp Tyr	
35 40 45	
Gly Leu Ile Gln Arg Leu Cys Glu Pro Glu Arg Gln Leu Ile Phe Arg	
50 55 60	
Val Pro Trp Val Asp Asp Asn Gly Gln Val His Val Asn Arg Gly Phe	
65 70 75 80	
Arg Val Gln Phe Asn Ser Ala Leu Gly Pro Tyr Lys Gly Gly Leu Arg	
85 90 95	
Phe His Pro Ser Val Asn Leu Gly Ile Val Lys Phe Leu Gly Phe Glu	
100 105 110	

Gln Ile Phe Lys Asn Ser Leu Thr Gly Leu Pro Ile Gly Gly Gly Lys
 115 120 125

Gly Gly Ser Asp Phe Asp Pro Lys Gly Lys Ser Glu Leu Glu Ile Met
 130 135 140

Arg Phe Cys Gln Ser Phe Met Thr Glu Leu His Arg His Ile Gly Glu
 145 150 155 160

Tyr Arg Asp Val Pro Ala Gly Asp Ile Gly Val Gly Gly Arg Glu Ile
 165 170 175

Gly Tyr Leu Phe Gly His Tyr Arg Arg Leu Ala Asn Gln His Glu Ser
 180 185 190

Gly Val Leu Thr Gly Lys Gly Leu Thr Trp Gly Gly Ser Leu Val Arg
 195 200 205

Thr Glu Ala Thr Gly Phe Gly Thr Val Tyr Phe Val Gln Glu Met Ile
 210 215 220

Lys Ala Glu Gly Glu Thr Leu Glu Gly Lys Lys Val Ile Val Ser Gly
 225 230 235 240

Ser Gly Asn Val Ala Thr Tyr Ala Ile Gln Lys Val Gln Glu Leu Gly
 245 250 255

Ala Val Val Val Gly Phe Ser Asp Ser Ser Gly Trp Val Ser Thr Pro
 260 265 270

Asn Gly Val Asp Val Ala Lys Leu Arg Glu Ile Lys Glu Val Arg Arg
 275 280 285

Ala Arg Val Ser Ser Tyr Ala Asp Glu Val Glu Gly Ala Glu Tyr His
 290 295 300

Thr Asp Gly Ser Ile Trp Asp Leu Thr Ala Asp Ile Ala Leu Pro Cys
 305 310 315 320

Ala Thr Gln Asn Glu Leu Asp Gly Asp Asn Ala Arg Thr Leu Ala Asp
 325 330 335

Asn Gly Cys Arg Phe Val Ala Glu Gly Ala Asn Met Pro Ser Thr Pro
 340 345 350

Glu Ala Ile Asp Val Phe Arg Glu Arg Gly Val Leu Phe Gly Pro Gly

355

360

365

Lys Ala Ala Asn Ala Gly Gly Val Ala Thr Ser Ala Leu Glu Met Gln
 370 375 380

Gln Asn Ala Ser Arg Asp Ser Trp Ser Phe Glu Tyr Thr Asp Glu Arg
 385 390 395 400

Leu His Arg Ile Met Lys Asn Ile Phe Lys Ser Cys Ala Asp Thr Ala
 405 410 415

Lys Glu Tyr Gly His Glu Lys Asn Tyr Val Val Gly Ala Asn Ile Ala
 420 425 430

Gly Phe Lys Lys Val Ala Asp Ala Met Leu Ala Gln Gly Val Ile
 435 440 445

<210> 102

<211> 1344

<212> DNA

<213> Brevibacterium lactofermentum

<220>

<221> CDS

<222> (1)..(1341)

<223>

<400> 102

atg aca gtt gat gag cag gtc tct aac tat tac gac atg ctt ctg aag 48
 Met Thr Val Asp Glu Gln Val Ser Asn Tyr Tyr Asp Met Leu Leu Lys
 1 5 10 15

cgc aat gct ggc gag cct gaa ttt cac cag gca gtg gca gag gtt ttg 96
 Arg Asn Ala Gly Glu Pro Glu Phe His Gln Ala Val Ala Glu Val Leu
 20 25 30

gaa tct ttg aag atc gtc ctg gaa aag gac cct cat tac gct gat tac 144
 Glu Ser Leu Lys Ile Val Leu Glu Lys Asp Pro His Tyr Ala Asp Tyr
 35 40 45

ggc ctc atc cag cgc ctg tgc gag cct gag cgt cag ctc atc ttc cgt 192
 Gly Leu Ile Gln Arg Leu Cys Glu Pro Glu Arg Gln Leu Ile Phe Arg
 50 55 60

gtg cct tgg gtt gat gac cag ggc cag gtc cac gtc aac cgt ggt ttc 240
 Val Pro Trp Val Asp Asp Gln Gly Gln Val His Val Asn Arg Gly Phe
 65 70 75 80

cgc gtg cag ttc aac tct gca ctt gga cca tac aag ggc ggc ctg cgc 288
 Arg Val Gln Phe Asn Ser Ala Leu Gly Pro Tyr Lys Gly Gly Leu Arg
 85 90 95

ttc cac cca tct gta aac ctg ggc att gtg aag ttc ctg ggc ttt gag 336
 Phe His Pro Ser Val Asn Leu Gly Ile Val Lys Phe Leu Gly Phe Glu
 100 105 110

cag atc ttt aaa aac tcc cta acc ggc ctg cca atc ggt ggt ggc aag	384
Gln Ile Phe Lys Asn Ser Leu Thr Gly Leu Pro Ile Gly Gly Gly Lys	
115 120 125	
ggt gga tcc gac ttc gac cct aag ggc aag tcc gat ctg gaa atc atg	432
Gly Gly Ser Asp Phe Asp Pro Lys Gly Lys Ser Asp Leu Glu Ile Met	
130 135 140	
cgt ttc tgc cag tcc ttc atg acc gag ctg cac cgc cac atc ggt gag	480
Arg Phe Cys Gln Ser Phe Met Thr Glu Leu His Arg His Ile Gly Glu	
145 150 155 160	
tac cgc gac gtt cct gca ggt gac atc gga gtt ggt ggc cgc gag atc	528
Tyr Arg Asp Val Pro Ala Gly Asp Ile Gly Val Gly Gly Arg Glu Ile	
165 170 175	
ggt tac ctg ttt ggc cac tac cgt cgc atg gct aac cag cac gag tcc	576
Gly Tyr Leu Phe Gly His Tyr Arg Arg Met Ala Asn Gln His Glu Ser	
180 185 190	
ggc gtt ttg acc ggt aag ggc ctg acc tgg ggt gga tcc ctg gtc cgc	624
Gly Val Leu Thr Gly Lys Gly Leu Thr Trp Gly Gly Ser Leu Val Arg	
195 200 205	
acc gag gca act ggc tac ggc tgc gtt tac ttc gtg agt gaa atg atc	672
Thr Glu Ala Thr Gly Tyr Gly Cys Val Tyr Phe Val Ser Glu Met Ile	
210 215 220	
aag gct aag ggc gag agc atc agc ggc cag aag atc atc gtt tcc ggt	720
Lys Ala Lys Gly Glu Ser Ile Ser Gly Gln Lys Ile Ile Val Ser Gly	
225 230 235 240	
tcc ggc aac gta gca acc tac gcg att gaa aag gct cag gaa ctc ggc	768
Ser Gly Asn Val Ala Thr Tyr Ala Ile Glu Lys Ala Gln Glu Leu Gly	
245 250 255	
gca acc gtt att ggt ttc tcc gat tcc agc ggt tgg gtt cat acc cct	816
Ala Thr Val Ile Gly Phe Ser Asp Ser Ser Gly Trp Val His Thr Pro	
260 265 270	
aac ggc gtt gac gtg gct aag ctc cgc gaa atc aag gaa gtt cgc cgc	864
Asn Gly Val Asp Val Ala Lys Leu Arg Glu Ile Lys Glu Val Arg Arg	
275 280 285	
gca cgc gta tcc gtg tac gcc gac gaa att gaa ggc gca acc tac cac	912
Ala Arg Val Ser Val Tyr Ala Asp Glu Ile Glu Gly Ala Thr Tyr His	
290 295 300	
acc gac ggt tcc atc tgg gat ctc aag tgc gat atc gct ctt cct tgt	960
Thr Asp Gly Ser Ile Trp Asp Leu Lys Cys Asp Ile Ala Leu Pro Cys	
305 310 315 320	
gca act cag aac gag ctc aac ggc gag aac gct aag act ctt gca gac	1008
Ala Thr Gln Asn Glu Leu Asn Gly Glu Asn Ala Lys Thr Leu Ala Asp	
325 330 335	
aac ggc tgc cgt ttc gtt gct gaa ggc gcg aac atg cct tcc acc cct	1056
Asn Gly Cys Arg Phe Val Ala Glu Gly Ala Asn Met Pro Ser Thr Pro	
340 345 350	

gag gct gtt gag gtc ttc cgt gag cgc gac atc cgc ttc gga cca ggc 1104
 Glu Ala Val Glu Val Phe Arg Glu Arg Asp Ile Arg Phe Gly Pro Gly
 355 360 365

aag gca gct aac gct ggt ggc gtt gca acc tcc gct ctg gag atg cag 1152
 Lys Ala Ala Asn Ala Gly Gly Val Ala Thr Ser Ala Leu Glu Met Gln
 370 375 380

cag aac gct tcg cgc gat tcc tgg agc ttc gag tac acc gac gag cgc 1200
 Gln Asn Ala Ser Arg Asp Ser Trp Ser Phe Glu Tyr Thr Asp Glu Arg
 385 390 395 400

ctc cag gtg atc atg aag aac atc ttc aag acc tgt gca gag acc gca 1248
 Leu Gln Val Ile Met Lys Asn Ile Phe Lys Thr Cys Ala Glu Thr Ala
 405 410 415

gca gag tat gga cac gag aac gat tac gtt gtc ggc gct aac att gct 1296
 Ala Glu Tyr Gly His Glu Asn Asp Tyr Val Val Gly Ala Asn Ile Ala
 420 425 430

ggc ttt aag aag gta gct gac gcg atg ctg gca cag ggc gtc atc taa 1344
 Gly Phe Lys Lys Val Ala Asp Ala Met Leu Ala Gln Gly Val Ile
 435 440 445

<210> 103

<211> 447

<212> PRT

<213> Brevibacterium lactofermentum

<400> 103

Met Thr Val Asp Glu Gln Val Ser Asn Tyr Tyr Asp Met Leu Leu Lys
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Arg Asn Ala Gly Glu Pro Glu Phe His Gln Ala Val Ala Glu Val Leu
 20 25 30

Glu Ser Leu Lys Ile Val Leu Glu Lys Asp Pro His Tyr Ala Asp Tyr
 35 40 45

Gly Leu Ile Gln Arg Leu Cys Glu Pro Glu Arg Gln Leu Ile Phe Arg
 50 55 60

Val Pro Trp Val Asp Asp Gln Gly Gln Val His Val Asn Arg Gly Phe
 65 70 75 80

Arg Val Gln Phe Asn Ser Ala Leu Gly Pro Tyr Lys Gly Gly Leu Arg
 85 90 95

Phe His Pro Ser Val Asn Leu Gly Ile Val Lys Phe Leu Gly Phe Glu
 100 105 110

Gln Ile Phe Lys Asn Ser Leu Thr Gly Leu Pro Ile Gly Gly Gly Lys

115							120									125
Gly	Gly	Ser	Asp	Phe	Asp	Pro	Lys	Gly	Lys	Ser	Asp	Leu	Glu	Ile	Met	
130						135					140					
Arg	Phe	Cys	Gln	Ser	Phe	Met	Thr	Glu	Leu	His	Arg	His	Ile	Gly	Glu	
145					150					155					160	
Tyr	Arg	Asp	Val	Pro	Ala	Gly	Asp	Ile	Gly	Val	Gly	Gly	Arg	Glu	Ile	
				165					170					175		
Gly	Tyr	Leu	Phe	Gly	His	Tyr	Arg	Arg	Met	Ala	Asn	Gln	His	Glu	Ser	
			180					185					190			
Gly	Val	Leu	Thr	Gly	Lys	Gly	Leu	Thr	Trp	Gly	Gly	Ser	Leu	Val	Arg	
		195					200					205				
Thr	Glu	Ala	Thr	Gly	Tyr	Gly	Cys	Val	Tyr	Phe	Val	Ser	Glu	Met	Ile	
	210					215					220					
Lys	Ala	Lys	Gly	Glu	Ser	Ile	Ser	Gly	Gln	Lys	Ile	Ile	Val	Ser	Gly	
225					230					235					240	
Ser	Gly	Asn	Val	Ala	Thr	Tyr	Ala	Ile	Glu	Lys	Ala	Gln	Glu	Leu	Gly	
				245					250					255		
Ala	Thr	Val	Ile	Gly	Phe	Ser	Asp	Ser	Ser	Gly	Trp	Val	His	Thr	Pro	
			260					265					270			
Asn	Gly	Val	Asp	Val	Ala	Lys	Leu	Arg	Glu	Ile	Lys	Glu	Val	Arg	Arg	
		275					280					285				
Ala	Arg	Val	Ser	Val	Tyr	Ala	Asp	Glu	Ile	Glu	Gly	Ala	Thr	Tyr	His	
	290					295					300					
Thr	Asp	Gly	Ser	Ile	Trp	Asp	Leu	Lys	Cys	Asp	Ile	Ala	Leu	Pro	Cys	
305					310					315					320	
Ala	Thr	Gln	Asn	Glu	Leu	Asn	Gly	Glu	Asn	Ala	Lys	Thr	Leu	Ala	Asp	
				325					330					335		
Asn	Gly	Cys	Arg	Phe	Val	Ala	Glu	Gly	Ala	Asn	Met	Pro	Ser	Thr	Pro	
			340					345					350			
Glu	Ala	Val	Glu	Val	Phe	Arg	Glu	Arg	Asp	Ile	Arg	Phe	Gly	Pro	Gly	
		355					360					365				

Lys Ala Ala Asn Ala Gly Gly Val Ala Thr Ser Ala Leu Glu Met Gln
 370 375 380

Gln Asn Ala Ser Arg Asp Ser Trp Ser Phe Glu Tyr Thr Asp Glu Arg
 385 390 395 400

Leu Gln Val Ile Met Lys Asn Ile Phe Lys Thr Cys Ala Glu Thr Ala
 405 410 415

Ala Glu Tyr Gly His Glu Asn Asp Tyr Val Val Gly Ala Asn Ile Ala
 420 425 430

Gly Phe Lys Lys Val Ala Asp Ala Met Leu Ala Gln Gly Val Ile
 435 440 445

<210> 104
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic DNA

<220>
 <221> misc_feature
 <222> (9)..(9)
 <223> n is inosine

<400> 104
 aagatcacnt acatcgaygg

20

<210> 105
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic DNA

<400> 105
 tagaagtcta cgttcgggta

20

<210> 106
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic DNA

<400> 106

gtcgacaata gcctgaatct g 21

<210> 107
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic DNA

<400> 107
 cggtggaacc ggtgctgaca t 21

<210> 108
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic DNA

<400> 108
 ggggtggggaa ttcggtcatg t 21

<210> 109
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic DNA

<400> 109
 tgtcgtagcc gcggtagcgc a 21

<210> 110
 <211> 1293
 <212> DNA
 <213> Corynebacterium thermoaminogenes

<220>
 <221> CDS
 <222> (1)..(1290)
 <223>

<400> 110
 gtg gct tct gat aac aac aag gct gta ctg cac tac cct ggc ggc gaa 48
 Val Ala Ser Asp Asn Asn Lys Ala Val Leu His Tyr Pro Gly Gly Glu
 1 5 10 15

ttc gag atg ggc atc aag cag gcc acc gag ggt aac tcc ggt gtc atc 96
 Phe Glu Met Gly Ile Lys Gln Ala Thr Glu Gly Asn Ser Gly Val Ile
 20 25 30

ctg ggt aag atg ctg tcg gaa acc ggt ctg gtc acc ttc gac ccc ggt 144
 Leu Gly Lys Met Leu Ser Glu Thr Gly Leu Val Thr Phe Asp Pro Gly
 35 40 45

tat gtc agc acc ggt tcc acc gaa tcc aag atc acc tac atc gat ggt Tyr Val Ser Thr Gly Ser Thr Glu Ser Lys Ile Thr Tyr Ile Asp Gly 50 55 60	192
gat gca ggc atc ctg cgc tac cgc ggc tac gac att gcg gat ctg gcc Asp Ala Gly Ile Leu Arg Tyr Arg Gly Tyr Asp Ile Ala Asp Leu Ala 65 70 75 80	240
gaa aat gcc acc ttc aat gag gtc tcc tac ctc ctg atc aag ggt gag Glu Asn Ala Thr Phe Asn Glu Val Ser Tyr Leu Leu Ile Lys Gly Glu 85 90 95	288
ctc ccg acc ccg gaa gag ctc cac aag ttc aac gac gag att cgt cac Leu Pro Thr Pro Glu Glu Leu His Lys Phe Asn Asp Glu Ile Arg His 100 105 110	336
cac acc ctg ctg gac gag gac ttc aag tcc cag ttc aat gtc ttc cct His Thr Leu Leu Asp Glu Asp Phe Lys Ser Gln Phe Asn Val Phe Pro 115 120 125	384
cgc gat gcc cac ccg atg gcc acc ctg gcc tcc tcg gtt aac atc ctc Arg Asp Ala His Pro Met Ala Thr Leu Ala Ser Ser Val Asn Ile Leu 130 135 140	432
tcc acc tac tac cag gat cag ctg gat ccc ctg gat gag gct cag ctg Ser Thr Tyr Tyr Gln Asp Gln Leu Asp Pro Leu Asp Glu Ala Gln Leu 145 150 155 160	480
gac aag gca acc gtc cgc ctg atg gcg aag gtt ccg atg ctg gct gca Asp Lys Ala Thr Val Arg Leu Met Ala Lys Val Pro Met Leu Ala Ala 165 170 175	528
tac gca cac cgt gcc cgc aag ggt gcg ccg tac atg tac ccg gac aac Tyr Ala His Arg Ala Arg Lys Gly Ala Pro Tyr Met Tyr Pro Asp Asn 180 185 190	576
tcc ctc aat gcc cgt gag aac ttc ctg cgc atg atg ttc ggt tac ccg Ser Leu Asn Ala Arg Glu Asn Phe Leu Arg Met Met Phe Gly Tyr Pro 195 200 205	624
acc gag ccg tac gag gtt gat ccg atc atg gtc aaa gcc ctc gac aag Thr Glu Pro Tyr Glu Val Asp Pro Ile Met Val Lys Ala Leu Asp Lys 210 215 220	672
ctg ctc atc ctg cac gca gac cac gag cag aac tgc tcc acc tcc act Leu Leu Ile Leu His Ala Asp His Glu Gln Asn Cys Ser Thr Ser Thr 225 230 235 240	720
gtc cgc atg atc ggc tcc gcg cag gcg aac atg ttc gtc tcc atc gcc Val Arg Met Ile Gly Ser Ala Gln Ala Asn Met Phe Val Ser Ile Ala 245 250 255	768
ggc ggc atc aac gca ctc tcc ggc ccg ctg cac ggt ggc gcc aac cag Gly Gly Ile Asn Ala Leu Ser Gly Pro Leu His Gly Gly Ala Asn Gln 260 265 270	816
gct gtc ctc gag atg ctc gag gag atc gca gcc aac ggc ggc gac gca Ala Val Leu Glu Met Leu Glu Glu Ile Ala Ala Asn Gly Gly Asp Ala 275 280 285	864

acc gac ttc atg aac cgc gtg aag aac aag gag aag ggt gtc cgc ctc 912
 Thr Asp Phe Met Asn Arg Val Lys Asn Lys Glu Lys Gly Val Arg Leu
 290 295 300

atg ggc ttc gga cac cgc gtc tac aag aac tac gat ccg cgt gca gcc 960
 Met Gly Phe Gly His Arg Val Tyr Lys Asn Tyr Asp Pro Arg Ala Ala
 305 310 315 320

atc gtc aag gac acc gcc cac gag atc ctc gag cac ctc ggt ggc gac 1008
 Ile Val Lys Asp Thr Ala His Glu Ile Leu Glu His Leu Gly Gly Asp
 325 330 335

cca ctg ctg gat ctg gct ctc aag ctg gaa gaa atc gca ctc aac gac 1056
 Pro Leu Leu Asp Leu Ala Leu Lys Leu Glu Glu Ile Ala Leu Asn Asp
 340 345 350

gat tac ttc atc tcc cgc aag ctg tac ccg aac gtg gac ttc tac acc 1104
 Asp Tyr Phe Ile Ser Arg Lys Leu Tyr Pro Asn Val Asp Phe Tyr Thr
 355 360 365

ggc ctg atc tac cgc gcc atg ggc ttc ccg acg gac ttc ttc acc gtc 1152
 Gly Leu Ile Tyr Arg Ala Met Gly Phe Pro Thr Asp Phe Phe Thr Val
 370 375 380

ctg ttc gcc atc ggc cgc ctc ccg ggc tgg atc gcc cac tac cgc gag 1200
 Leu Phe Ala Ile Gly Arg Leu Pro Gly Trp Ile Ala His Tyr Arg Glu
 385 390 395 400

cag ctc gcc gat ccg ggc gcc aag atc aac cgt cct cgc cag atc tac 1248
 Gln Leu Ala Asp Pro Gly Ala Lys Ile Asn Arg Pro Arg Gln Ile Tyr
 405 410 415

acc ggt gag acc gca cgc aag atc atc ccc cgc gaa gag cgc tag 1293
 Thr Gly Glu Thr Ala Arg Lys Ile Ile Pro Arg Glu Glu Arg
 420 425 430

<210> 111
 <211> 430
 <212> PRT
 <213> *Corynebacterium thermoaminogenes*

<400> 111

Val Ala Ser Asp Asn Asn Lys Ala Val Leu His Tyr Pro Gly Gly Glu
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Phe Glu Met Gly Ile Lys Gln Ala Thr Glu Gly Asn Ser Gly Val Ile
 20 25 30

Leu Gly Lys Met Leu Ser Glu Thr Gly Leu Val Thr Phe Asp Pro Gly
 35 40 45

Tyr Val Ser Thr Gly Ser Thr Glu Ser Lys Ile Thr Tyr Ile Asp Gly
 50 55 60

Asp Ala Gly Ile Leu Arg Tyr Arg Gly Tyr Asp Ile Ala Asp Leu Ala

65					70						75				80
Glu	Asn	Ala	Thr	Phe	Asn	Glu	Val	Ser	Tyr	Leu	Leu	Ile	Lys	Gly	Glu
				85					90					95	
Leu	Pro	Thr	Pro	Glu	Glu	Leu	His	Lys	Phe	Asn	Asp	Glu	Ile	Arg	His
			100					105					110		
His	Thr	Leu	Leu	Asp	Glu	Asp	Phe	Lys	Ser	Gln	Phe	Asn	Val	Phe	Pro
		115					120					125			
Arg	Asp	Ala	His	Pro	Met	Ala	Thr	Leu	Ala	Ser	Ser	Val	Asn	Ile	Leu
	130					135					140				
Ser	Thr	Tyr	Tyr	Gln	Asp	Gln	Leu	Asp	Pro	Leu	Asp	Glu	Ala	Gln	Leu
145					150				155						160
Asp	Lys	Ala	Thr	Val	Arg	Leu	Met	Ala	Lys	Val	Pro	Met	Leu	Ala	Ala
				165					170					175	
Tyr	Ala	His	Arg	Ala	Arg	Lys	Gly	Ala	Pro	Tyr	Met	Tyr	Pro	Asp	Asn
			180					185					190		
Ser	Leu	Asn	Ala	Arg	Glu	Asn	Phe	Leu	Arg	Met	Met	Phe	Gly	Tyr	Pro
		195					200					205			
Thr	Glu	Pro	Tyr	Glu	Val	Asp	Pro	Ile	Met	Val	Lys	Ala	Leu	Asp	Lys
	210					215					220				
Leu	Leu	Ile	Leu	His	Ala	Asp	His	Glu	Gln	Asn	Cys	Ser	Thr	Ser	Thr
225					230					235					240
Val	Arg	Met	Ile	Gly	Ser	Ala	Gln	Ala	Asn	Met	Phe	Val	Ser	Ile	Ala
				245					250					255	
Gly	Gly	Ile	Asn	Ala	Leu	Ser	Gly	Pro	Leu	His	Gly	Gly	Ala	Asn	Gln
			260					265					270		
Ala	Val	Leu	Glu	Met	Leu	Glu	Glu	Ile	Ala	Ala	Asn	Gly	Gly	Asp	Ala
		275					280					285			
Thr	Asp	Phe	Met	Asn	Arg	Val	Lys	Asn	Lys	Glu	Lys	Gly	Val	Arg	Leu
	290					295					300				
Met	Gly	Phe	Gly	His	Arg	Val	Tyr	Lys	Asn	Tyr	Asp	Pro	Arg	Ala	Ala
305					310					315					320

Ile Val Lys Asp Thr Ala His Glu Ile Leu Glu His Leu Gly Gly Asp
 325 330 335

Pro Leu Leu Asp Leu Ala Leu Lys Leu Glu Glu Ile Ala Leu Asn Asp
 340 345 350

Asp Tyr Phe Ile Ser Arg Lys Leu Tyr Pro Asn Val Asp Phe Tyr Thr
 355 360 365

Gly Leu Ile Tyr Arg Ala Met Gly Phe Pro Thr Asp Phe Phe Thr Val
 370 375 380

Leu Phe Ala Ile Gly Arg Leu Pro Gly Trp Ile Ala His Tyr Arg Glu
 385 390 395 400

Gln Leu Ala Asp Pro Gly Ala Lys Ile Asn Arg Pro Arg Gln Ile Tyr
 405 410 415

Thr Gly Glu Thr Ala Arg Lys Ile Ile Pro Arg Glu Glu Arg
 420 425 430

<210> 112

<211> 1314

<212> DNA

<213> Brevibacterium lactofermentum

<220>

<221> CDS

<222> (1)..(1311)

<223>

<400> 112

atg	ttt	gaa	agg	gat	atc	gtg	gct	act	gat	aac	aac	aag	gct	gtc	ctg	48
Met	Phe	Glu	Arg	Asp	Ile	Val	Ala	Thr	Asp	Asn	Asn	Lys	Ala	Val	Leu	
1			5					10					15			

cac	tac	ccc	ggt	ggc	gag	ttc	gaa	atg	gac	atc	atc	gag	gct	tct	gag	96
His	Tyr	Pro	Gly	Gly	Glu	Phe	Glu	Met	Asp	Ile	Ile	Glu	Ala	Ser	Glu	
		20						25				30				

ggt	aac	aac	ggt	gtt	gtc	ctg	ggc	aag	atg	ctg	tct	gag	act	gga	ctg	144
Gly	Asn	Asn	Gly	Val	Val	Leu	Gly	Lys	Met	Leu	Ser	Glu	Thr	Gly	Leu	
	35					40					45					

atc	act	ttt	gac	cca	ggt	tat	gtg	agc	act	ggc	tcc	acc	gag	tcg	aag	192
Ile	Thr	Phe	Asp	Pro	Gly	Tyr	Val	Ser	Thr	Gly	Ser	Thr	Glu	Ser	Lys	
	50				55					60						

atc	acc	tac	atc	gat	ggc	gat	gcg	gga	atc	ctg	cgt	tac	cgc	ggc	tat	240
Ile	Thr	Tyr	Ile	Asp	Gly	Asp	Ala	Gly	Ile	Leu	Arg	Tyr	Arg	Gly	Tyr	
65					70					75				80		

gac atc gct gat ctg gct gag aat gcc acc ttc aac gag gtt tct tac	288
Asp Ile Ala Asp Leu Ala Glu Asn Ala Thr Phe Asn Glu Val Ser Tyr	
85 90 95	
cta ctt atc aac ggt gaa cta cca acc cca gat gag ctt cac aag ttt	336
Leu Leu Ile Asn Gly Glu Leu Pro Thr Pro Asp Glu Leu His Lys Phe	
100 105 110	
aac gac gag att cgc cac cac acc ctt ctg gac gag gac ttc aag tcc	384
Asn Asp Glu Ile Arg His His Thr Leu Leu Asp Glu Asp Phe Lys Ser	
115 120 125	
cag ttc aac gtg ttc cca cgc gac gct cac cca atg gca acc ttg gct	432
Gln Phe Asn Val Phe Pro Arg Asp Ala His Pro Met Ala Thr Leu Ala	
130 135 140	
tcc tcg gtt aac att ttg tct acc tac tac cag gat cag ctg aac cca	480
Ser Ser Val Asn Ile Leu Ser Thr Tyr Tyr Gln Asp Gln Leu Asn Pro	
145 150 155 160	
ctc gat gag gca cag ctt gat aag gca acc gtt cgc ctc atg gca aag	528
Leu Asp Glu Ala Gln Leu Asp Lys Ala Thr Val Arg Leu Met Ala Lys	
165 170 175	
gtt cca atg ctg gct gcg tac gca cac cgc gca cgc aag ggt gct cct	576
Val Pro Met Leu Ala Ala Tyr Ala His Arg Ala Arg Lys Gly Ala Pro	
180 185 190	
tac atg tac cca gac aac tcc ctc aac gcg cgt gag aac ttc ctg cgc	624
Tyr Met Tyr Pro Asp Asn Ser Leu Asn Ala Arg Glu Asn Phe Leu Arg	
195 200 205	
atg atg ttc ggt tac cca acc gag cca tac gag atc gac cca atc atg	672
Met Met Phe Gly Tyr Pro Thr Glu Pro Tyr Glu Ile Asp Pro Ile Met	
210 215 220	
gtc aag gct ctg gac aag ctg ctc atc ctg cac gct gac cac gag cag	720
Val Lys Ala Leu Asp Lys Leu Leu Ile Leu His Ala Asp His Glu Gln	
225 230 235 240	
aac tgc tcc acc tcc acc gtt cgt atg atc ggt tcc gca cag gcc aac	768
Asn Cys Ser Thr Ser Thr Val Arg Met Ile Gly Ser Ala Gln Ala Asn	
245 250 255	
atg ttt gtc tcc atc gct ggt ggc atc aac gct ctg tcc ggc cca ctg	816
Met Phe Val Ser Ile Ala Gly Gly Ile Asn Ala Leu Ser Gly Pro Leu	
260 265 270	
cac ggt ggc gca aac cag gct gtt ctg gag atg ctc gaa gac atc aag	864
His Gly Gly Ala Asn Gln Ala Val Leu Glu Met Leu Glu Asp Ile Lys	
275 280 285	
aac aac cac ggt ggc gac gca acc gcg ttc atg aac aag gtc aag aac	912
Asn Asn His Gly Gly Asp Ala Thr Ala Phe Met Asn Lys Val Lys Asn	
290 295 300	
aag gaa gac ggc gtc cgc ctc atg ggc ttc gga cac cgc gtt tac aag	960
Lys Glu Asp Gly Val Arg Leu Met Gly Phe Gly His Arg Val Tyr Lys	
305 310 315 320	
aac tac gat cca cgt gca gca atc gtc aag gag acc gca cac gag atc	1008

Asn Tyr Asp Pro Arg Ala Ala Ile Val Lys Glu Thr Ala His Glu Ile
 325 330 335
 ctc gag cac ctc ggt ggc gac gat ctt ctg gat ctg gca atc aag ctg 1056
 Leu Glu His Leu Gly Gly Asp Asp Leu Leu Asp Leu Ala Ile Lys Leu
 340 345 350
 gaa gaa att gca ctg gct gat gat tac ttc atc tcc cgc aag ctc tac 1104
 Glu Glu Ile Ala Leu Ala Asp Asp Tyr Phe Ile Ser Arg Lys Leu Tyr
 355 360 365
 ccg aac gta gac ttc tac acc ggc ctg atc tac cgc gca atg ggc ttc 1152
 Pro Asn Val Asp Phe Tyr Thr Gly Leu Ile Tyr Arg Ala Met Gly Phe
 370 375 380
 cca act gac ttc ttc acc gta ttg ttc gca atc ggt cgt ctg cca gga 1200
 Pro Thr Asp Phe Phe Thr Val Leu Phe Ala Ile Gly Arg Leu Pro Gly
 385 390 395 400
 tgg atc gct cac tac cgc gag cag ctc ggt gca gca ggc aac aag atc 1248
 Trp Ile Ala His Tyr Arg Glu Gln Leu Gly Ala Ala Gly Asn Lys Ile
 405 410 415
 aac cgc cca cgc cag gtc tac acc ggc aag gaa tcc cgc aag ttg gtt 1296
 Asn Arg Pro Arg Gln Val Tyr Thr Gly Lys Glu Ser Arg Lys Leu Val
 420 425 430
 cct cgc gag gag cgc taa 1314
 Pro Arg Glu Arg
 435

<210> 113
 <211> 437
 <212> PRT
 <213> Brevibacterium lactofermentum

<400> 113

Met Phe Glu Arg Asp Ile Val Ala Thr Asp Asn Asn Lys Ala Val Leu
 1 5 10 15

His Tyr Pro Gly Gly Glu Phe Glu Met Asp Ile Ile Glu Ala Ser Glu
 20 25 30

Gly Asn Asn Gly Val Val Leu Gly Lys Met Leu Ser Glu Thr Gly Leu
 35 40 45

Ile Thr Phe Asp Pro Gly Tyr Val Ser Thr Gly Ser Thr Glu Ser Lys
 50 55 60

Ile Thr Tyr Ile Asp Gly Asp Ala Gly Ile Leu Arg Tyr Arg Gly Tyr
 65 70 75 80

Asp Ile Ala Asp Leu Ala Glu Asn Ala Thr Phe Asn Glu Val Ser Tyr
 85 90 95

Leu Leu Ile Asn Gly Glu Leu Pro Thr Pro Asp Glu Leu His Lys Phe
 100 105 110

Asn Asp Glu Ile Arg His His Thr Leu Leu Asp Glu Asp Phe Lys Ser
 115 120 125

Gln Phe Asn Val Phe Pro Arg Asp Ala His Pro Met Ala Thr Leu Ala
 130 135 140

Ser Ser Val Asn Ile Leu Ser Thr Tyr Tyr Gln Asp Gln Leu Asn Pro
 145 150 155 160

Leu Asp Glu Ala Gln Leu Asp Lys Ala Thr Val Arg Leu Met Ala Lys
 165 170 175

Val Pro Met Leu Ala Ala Tyr Ala His Arg Ala Arg Lys Gly Ala Pro
 180 185 190

Tyr Met Tyr Pro Asp Asn Ser Leu Asn Ala Arg Glu Asn Phe Leu Arg
 195 200 205

Met Met Phe Gly Tyr Pro Thr Glu Pro Tyr Glu Ile Asp Pro Ile Met
 210 215 220

Val Lys Ala Leu Asp Lys Leu Leu Ile Leu His Ala Asp His Glu Gln
 225 230 235 240

Asn Cys Ser Thr Ser Thr Val Arg Met Ile Gly Ser Ala Gln Ala Asn
 245 250 255

Met Phe Val Ser Ile Ala Gly Gly Ile Asn Ala Leu Ser Gly Pro Leu
 260 265 270

His Gly Gly Ala Asn Gln Ala Val Leu Glu Met Leu Glu Asp Ile Lys
 275 280 285

Asn Asn His Gly Gly Asp Ala Thr Ala Phe Met Asn Lys Val Lys Asn
 290 295 300

Lys Glu Asp Gly Val Arg Leu Met Gly Phe Gly His Arg Val Tyr Lys
 305 310 315 320

Asn Tyr Asp Pro Arg Ala Ala Ile Val Lys Glu Thr Ala His Glu Ile
 325 330 335

Leu Glu His Leu Gly Gly Asp Asp Leu Leu Asp Leu Ala Ile Lys Leu
 340 345 350

Glu Glu Ile Ala Leu Ala Asp Asp Tyr Phe Ile Ser Arg Lys Leu Tyr
 355 360 365

Pro Asn Val Asp Phe Tyr Thr Gly Leu Ile Tyr Arg Ala Met Gly Phe
 370 375 380

Pro Thr Asp Phe Phe Thr Val Leu Phe Ala Ile Gly Arg Leu Pro Gly
 385 390 395 400

Trp Ile Ala His Tyr Arg Glu Gln Leu Gly Ala Ala Gly Asn Lys Ile
 405 410 415

Asn Arg Pro Arg Gln Val Tyr Thr Gly Lys Glu Ser Arg Lys Leu Val
 420 425 430

Pro Arg Glu Glu Arg
 435

<210> 114
 <211> 1656
 <212> DNA
 <213> Corynebacterium thermoaminogenes

<220>
 <221> CDS
 <222> (309)..(1595)
 <223>

<400> 114
 acgcccgatt cttcaacact atcgaagagg tcccaaccga cgcgttgacc cagggcttgg 60
 gtactttgtc ccgcgcgcaa aatatcgtgt tgggtggcaac tggccaagga aaagcagaca 120
 gccatccgcg gaactgtgga aggtccagtg actgcttctt gcccaggttc cattctgcaa 180
 atgcacaaca acgccaccat catcgttgat gaagcagcag catccaagct gaaaaatgct 240
 gaccattacc gtctcatgga gcaattaaag ctgcgctaga aacaaaaagg aaagtactgt 300
 gtgggggt atg cac aca gaa ctt tcc agt ttg cgc cct gcg tac cat gtg 350
 Met His Thr Glu Leu Ser Ser Leu Arg Pro Ala Tyr His Val
 1 5 10
 act cct ccg cag ggc aga ctc aat gat ccc aat gga atg tac gtc gat 398
 Thr Pro Pro Gln Gly Arg Leu Asn Asp Pro Asn Gly Met Tyr Val Asp
 15 20 25 30
 gga gat acc ctc cac gtc tac tac cag cac gat cca ggt ttc ccc ttc 446
 Gly Asp Thr Leu His Val Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe
 35 40 45

gca cca aag cgc acc ggt tgg gct cac acc acc acg ccg ttg acc gga Ala Pro Lys Arg Thr Gly Trp Ala His Thr Thr Thr Pro Leu Thr Gly 50 55 60	494
ccg cag cga ttg cag tgg acg cac ctg ccc gat gct ctt tac ccg gat Pro Gln Arg Leu Gln Trp Thr His Leu Pro Asp Ala Leu Tyr Pro Asp 65 70 75	542
gta tcc tat gac ctg gat gga tgc tat tcc ggc gga gcc gta ttt tct Val Ser Tyr Asp Leu Asp Gly Cys Tyr Ser Gly Gly Ala Val Phe Ser 80 85 90	590
gac ggc acg ctt aaa ctt ttc tac acc ggc aac cga aaa att gac ggc Asp Gly Thr Leu Lys Leu Phe Tyr Thr Gly Asn Arg Lys Ile Asp Gly 95 100 105 110	638
aag cgc cgc gcc acc caa aac ctc gtc gaa gtc gag gac cca act ggg Lys Arg Arg Ala Thr Gln Asn Leu Val Glu Val Glu Asp Pro Thr Gly 115 120 125	686
ctg atg ggc ggc att cat cgc cgc tcg cct aaa aat ccg ctt atc gac Leu Met Gly Gly Ile His Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp 130 135 140	734
gga ccc gcc agc ggt ttt acg ccc cac tac cgc gat ccc atg atc agc Gly Pro Ala Ser Gly Phe Thr Pro His Tyr Arg Asp Pro Met Ile Ser 145 150 155	782
cct gat ggg gat ggt tgg aag atg gtt ctt ggg gct cag cgc gaa aac Pro Asp Gly Asp Gly Trp Lys Met Val Leu Gly Ala Gln Arg Glu Asn 160 165 170	830
ctc acc ggt gca gcg gtt cta tac cgc tcg gca gat ctt gaa aac tgg Leu Thr Gly Ala Ala Val Leu Tyr Arg Ser Ala Asp Leu Glu Asn Trp 175 180 185 190	878
gaa ttc tcc ggt gaa atc acc ttt gac ctc agc gac gca caa cct ggt Glu Phe Ser Gly Glu Ile Thr Phe Asp Leu Ser Asp Ala Gln Pro Gly 195 200 205	926
tct gcc cct gat ctc gtt cct ggc ggc tac atg tgg gaa tgc ccc aac Ser Ala Pro Asp Leu Val Pro Gly Gly Tyr Met Trp Glu Cys Pro Asn 210 215 220	974
ctt ttt acg ctt cgc gat gaa aaa acc ggc gaa gac ctc gat gtg ctg Leu Phe Thr Leu Arg Asp Glu Lys Thr Gly Glu Asp Leu Asp Val Leu 225 230 235	1022
att ttc tgt cca caa gga ttg gac cgt atc gat gat gag gtt act cac Ile Phe Cys Pro Gln Gly Leu Asp Arg Ile Asp Asp Glu Val Thr His 240 245 250	1070
tac gca agc tct gac cag tgc gga tat gtc gtc ggc aag ctt gaa gaa Tyr Ala Ser Ser Asp Gln Cys Gly Tyr Val Val Gly Lys Leu Glu Glu 255 260 265 270	1118
acg acc ttc cgt gtc ctg cga gga ttc agc gag ctg gat ttc ggt cat Thr Thr Phe Arg Val Leu Arg Gly Phe Ser Glu Leu Asp Phe Gly His 275 280 285	1166

gaa ttc tac gcg ccg cag gtt gca gtc aac ggt tcc gat gcc tgg ctt 1214
 Glu Phe Tyr Ala Pro Gln Val Ala Val Asn Gly Ser Asp Ala Trp Leu
 290 295 300
 gtg ggc tgg atg gga ttg cct gca cag gat gat cac cca aca gtt gcg 1262
 Val Gly Trp Met Gly Leu Pro Ala Gln Asp Asp His Pro Thr Val Ala
 305 310 315
 cag gaa gga tgg gtg cac tgc ctg acc gtt cct cgc agg ctt cat ttg 1310
 Gln Glu Gly Trp Val His Cys Leu Thr Val Pro Arg Arg Leu His Leu
 320 325 330
 cgt aac cat gcg atc tat caa gag ctt ctt ctc cca gaa ggg gag tcg 1358
 Arg Asn His Ala Ile Tyr Gln Glu Leu Leu Leu Pro Glu Gly Glu Ser
 335 340 345 350
 ggg gta act aga tct gta tta ggt tct gaa cct gtc cga gta gac atc 1406
 Gly Val Thr Arg Ser Val Leu Gly Ser Glu Pro Val Arg Val Asp Ile
 355 360 365
 cga gac aat gtt tcc ctc gag tgg gat ggt gtc cgg ttg tct gtg gat 1454
 Arg Asp Asn Val Ser Leu Glu Trp Asp Gly Val Arg Leu Ser Val Asp
 370 375 380
 cgc gat ggc gat cgt cgt gta gct gaa gta aaa cct ggc gaa tta gtg 1502
 Arg Asp Gly Asp Arg Arg Val Ala Glu Val Lys Pro Gly Glu Leu Val
 385 390 395
 atc gcg gac gat aat aca gcg att gag ata aca gca ggt cat ggc cag 1550
 Ile Ala Asp Asp Asn Thr Ala Ile Glu Ile Thr Ala Gly His Gly Gln
 400 405 410
 gtt tcc ttc gct ttc cgc acc ttc aaa ggt gac act att gag aga 1595
 Val Ser Phe Ala Phe Arg Thr Phe Lys Gly Asp Thr Ile Glu Arg
 415 420 425
 taagtcataa aaaagggcct tctgtggcgg attgtacaaa tacttcgcaa aatcccttga 1655
 t 1656

<210> 115
 <211> 429
 <212> PRT
 <213> Corynebacterium thermoaminogenes

<400> 115

Met His Thr Glu Leu Ser Ser Leu Arg Pro Ala Tyr His Val Thr Pro
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Pro Gln Gly Arg Leu Asn Asp Pro Asn Gly Met Tyr Val Asp Gly Asp
 20 25 30

Thr Leu His Val Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro
 35 40 45

Lys Arg Thr Gly Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln

50 55 60
 Arg Leu Gln Trp Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Val Ser
 65 70 75 80
 Tyr Asp Leu Asp Gly Cys Tyr Ser Gly Gly Ala Val Phe Ser Asp Gly
 85 90 95
 Thr Leu Lys Leu Phe Tyr Thr Gly Asn Arg Lys Ile Asp Gly Lys Arg
 100 105 110
 Arg Ala Thr Gln Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met
 115 120 125
 Gly Gly Ile His Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro
 130 135 140
 Ala Ser Gly Phe Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp
 145 150 155 160
 Gly Asp Gly Trp Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr
 165 170 175
 Gly Ala Ala Val Leu Tyr Arg Ser Ala Asp Leu Glu Asn Trp Glu Phe
 180 185 190
 Ser Gly Glu Ile Thr Phe Asp Leu Ser Asp Ala Gln Pro Gly Ser Ala
 195 200 205
 Pro Asp Leu Val Pro Gly Gly Tyr Met Trp Glu Cys Pro Asn Leu Phe
 210 215 220
 Thr Leu Arg Asp Glu Lys Thr Gly Glu Asp Leu Asp Val Leu Ile Phe
 225 230 235 240
 Cys Pro Gln Gly Leu Asp Arg Ile Asp Asp Glu Val Thr His Tyr Ala
 245 250 255
 Ser Ser Asp Gln Cys Gly Tyr Val Val Gly Lys Leu Glu Glu Thr Thr
 260 265 270
 Phe Arg Val Leu Arg Gly Phe Ser Glu Leu Asp Phe Gly His Glu Phe
 275 280 285
 Tyr Ala Pro Gln Val Ala Val Asn Gly Ser Asp Ala Trp Leu Val Gly
 290 295 300

Trp Met Gly Leu Pro Ala Gln Asp Asp His Pro Thr Val Ala Gln Glu
305 310 315 320

Gly Trp Val His Cys Leu Thr Val Pro Arg Arg Leu His Leu Arg Asn
325 330 335

His Ala Ile Tyr Gln Glu Leu Leu Leu Pro Glu Gly Glu Ser Gly Val
340 345 350

Thr Arg Ser Val Leu Gly Ser Glu Pro Val Arg Val Asp Ile Arg Asp
355 360 365

Asn Val Ser Leu Glu Trp Asp Gly Val Arg Leu Ser Val Asp Arg Asp
370 375 380

Gly Asp Arg Arg Val Ala Glu Val Lys Pro Gly Glu Leu Val Ile Ala
385 390 395 400

Asp Asp Asn Thr Ala Ile Glu Ile Thr Ala Gly His Gly Gln Val Ser
405 410 415

Phe Ala Phe Arg Thr Phe Lys Gly Asp Thr Ile Glu Arg
420 425

<210> 116
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic DNA

<400> 116
gtacatatg tcgtagaac gcgtaatacg actca 35

<210> 117
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic DNA

<400> 117
cgtagaacg cgtaatacga ctactatag ggaga 35

<210> 118
<211> 30
<212> DNA

<213> Artificial Sequence
 <220>
 <223> synthetic DNA
 <400> 118
 gtaaagagcg tcgggcaggt gcgtccactg 30

<210> 119
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> synthetic DNA
 <400> 119
 ggtgtgagcc cagccggtgc gctttggtgc 30

<210> 120
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> synthetic DNA
 <400> 120
 atcagccctg atggtgatgg ttggaaaatg 30

<210> 121
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> synthetic DNA
 <400> 121
 ggtgcagcgg ttctataccg ctcgacagat 30

<210> 122
 <211> 32
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> synthetic DNA
 <400> 122
 ggcccgggac gcccgattct tcaacactat cg 32

<210> 123
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic DNA

 <400> 123
 ggccccgggga tcaagggatt ttgcgaagta tt 32

<210> 124
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic DNA

 <400> 124
 gaagatctct atgaccagcg catcaagctg 30

<210> 125
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic DNA

 <400> 125
 gaagatctgg tcatcccaga acctgatcac 30

<210> 126
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic DNA

 <400> 126
 gcgcctgcag gtccgagggt gtgcgttcgg ca 32

<210> 127
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic DNA

 <400> 127
 gcgcctgcag gcaccaggat gccctcaacc ag 32

<210> 128
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>

<223> synthetic DNA

<400> 128

gggggtaccga tcactataac cccacagcac

30

<210> 129

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic DNA

<400> 129

gggggtaccct ggctgatctg aactaggcgc

30